

C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 02-Nov-2001  
C/Accession: E97919  
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Biaszczak, L.; Burgett, S.; Dehoff, B.S.; E  
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain Re.  
A:Reference number: A97872; M01D:21429245; PMID:11544234  
A/Accession: E97919  
A/Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-243 <KUR>  
A/Cross-references: GB:AE007317; PID:AK99185.1; PID:g15457942; GSPDB:GN00174  
C/Genetics:  
A:Gene: fabG  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
C:Keywords: oxidoreductase

Query Match 24.9%; Score 326.5; DB 2; Length 243;  
Best Local Similarity 35.1%; Pred. No. 1.9e-18;  
Matches 86; Conservative 36; Mismatches 104; Indels 23; Gaps 6;  
OY 15 ITGASGGLATAEERLVGOGASAVLLDLPNSGGE-----AQAKKLGNNCVFAPADVTSE 68  
DB 10 ITGSSRGIGLAIARHFAQAGANIVL-----NSRGAISELLAEFSNYGIRKVPISGDVSDF 65  
OY 69 KDVOATALAKGKRGVAVNAGIAVASKTYLKKQGTHTLDEDFORVLDVNLMTGFNV 128  
DB 66 ADARHMDQALAEIGSDVVLNNNGI--TQDTLMK-----TEADFEKVLKYNLTGAFNM 119  
OY 129 IRLVAGGQNEPDGOGGVINTASYAAFEQVGAASAKSGGIVGMLPIAPDLAP 188  
DB 120 TQSVL-----KPMKARAGAIINMSVVGMLGNIGQANVAAAGLIGFTKSVAREVAS 173  
OY 189 IGRVMTAPGLFGFPLTSLPEKVCNPLASQVPPSPRLGPAEVAHLVQAIENPFLNG 248  
DB 174 RNIRNVNAPGMIESDMTAISDKIKETLAQIPW-KEFGAEQVADLTVPFLAGQDYLTG 232  
OY 249 EVIRLDGAIRM 259  
DB 233 QVAIDGGLSM 243

RESULT 20  
G95048  
3-oxoacyl-[acyl-carrier protein] reductase [imported] - Streptococcus pneumoniae (strain  
C/Species: Streptococcus pneumoniae  
C/Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001  
C/Accession: G95048  
R/Bretlein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Reed, T.D.; Peterson, S.; Heid  
on, J.D.; Unayem, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; M01D:21357209; PMID:11463916  
A/Accession: G95048  
A/Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-243 <KUR>  
A/Cross-references: GB:AE005672; PID:NAK74584.1; PID:g14971891; GSPDB:GN00164; TIGR:SP4  
A:Experimental source: strain TIGR4  
C/Genetics:  
A:Gene: SP0421  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.9%; Score 325.5; DB 2; Length 243;  
Best Local Similarity 34.7%; Pred. No. 2.3e-18;  
Matches 87; Conservative 37; Mismatches 104; Indels 23; Gaps 6;  
OY 15 ITGASGGLATAEERLVGOGASAVLLDLPNSGGE-----AQAKKLGNNCVFAPADVTSE 68  
DB 10 ITGSSRGIGLAIARHFAQAGANIVL-----NSRGAISELLAEFSNYGIRKVPISGDVSDF 65

DB 10 ITGSSRGIGLAIARHFAQAGANIVL-----NSRGAISELLAEFSNYGIRKVPISGDVSDF 65  
OY 69 KDVOATALAKGKRGVAVNAGIAVASKTYLKKQGTHTLDEDFORVLDVNLMTGFNV 128  
DB 66 ADARHMDQALAEIGSDVVLNNNGI--TQDTLMK-----TEADFEKVLKYNLTGAFNM 119  
OY 129 IRLVAGGQNEPDGOGGVINTASYAAFEQVGAASAKSGGIVGMLPIAPDLAP 188  
DB 120 TQSVL-----KPMKARAGAIINMSVVGMLGNIGQANVAAAGLIGFTKSVAREVAS 173  
OY 189 IGRVMTAPGLFGFPLTSLPEKVCNPLASQVPPSPRLGPAEVAHLVQAIENPFLNG 248  
DB 174 RNIRNVNAPGMIESDMTAISDKIKETLAQIPW-KEFGAEQVADLTVPFLAGQDYLTG 232  
OY 249 EVIRLDGAIRM 259  
DB 233 QVAIDGGLSM 243

RESULT 21  
F86721  
hypothetical protein fabG [imported] - Lactococcus lactis subsp. lactis (strain IL14  
C/Species: Lactococcus lactis subsp. lactis  
C/Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C/Accession: F86721  
R/Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Eh  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
A:Reference number: A86625; M01D:21235186; PMID:11337471  
A/Accession: F86721  
A/Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-243 <STO>  
A/Cross-references: GB:AE005176; PID:g12723693; PID:NAK04872.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C/Genetics:  
A:Gene: fabG1  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.8%; Score 324.5; DB 2; Length 243;  
Best Local Similarity 31.7%; Pred. No. 2.7e-18;  
Matches 82; Conservative 48; Mismatches 104; Indels 25; Gaps 6;  
OY 8 VKGLVAVITGASGGLATAEERLVGOGASAVLLDLPNSGGEAQAKL-----GNNCVF 60  
DB 3 IRKNKNEVFGSTRGKATALPFAKAGSNLI-----NGRSAISELLAEFTAGVKAAG 57  
OY 61 APADVTSEKDVOATALAKGKRGVAVNAGIAVASKTYLKKQGTHTLDEDFORVLDV 120  
DB 58 ISGDISSEDAKQVMAEAFETLGSVDILVNNAGI--TRGSLTKSE-----EDFESVLT 111  
OY 121 NMGTFNVNIRLVAGGQNEPDGOGGVINTASYAAFEQVGAASAKSGGIVGML 180  
DB 112 NMGAFNMQAVL-----KPMRARSAGAIINMSVVGMLGNIGQANVAAAGLIGLTK 165  
OY 181 PIAPDLAPIGRVTAPGLFGFPLTSLPEKVCNPLASQVPPSPRLGPAEVAHLVQAI 240  
DB 166 SIAREVAARVRVNAVAPGIESDMTEVLSDKVAKMQQIPW-KRFGMEPELTATATQFL 224  
OY 241 IENPFLNGEVRIRLDGAIRM 259  
DB 225 AEOEYMGQVLTITDGVSM 243

RESULT 22  
T36846  
probable dehydrogenase - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 11-Jan-2000  
C/Accession: T36846  
R/Oliver, K.; Harris, D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1998  
A:Reference number: Z21615

Db 295 VEFLLAINPASSVYTGCVFTIDGGKTM 320

RESULT 16

C83961

C3-oxoacyl-(acyl-carrier protein) reductase fabG [imported] - *Bacillus halodurans* (strain C:Species: *Bacillus halodurans*

C:Date: 01-Dec-2000 #sequence.revision 01-Dec-2000 #text\_change 03-Aug-2001

C:Accession: C83961

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasak, R.; Masui, N.; Fujii, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: C83961

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-246 <STO>

A:Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BA06210.1; GSPD:GN000

A:Experimental source: strain C-125

C:Gene(s):

A:Gene: fabG

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match	25.5%	Score	333.5	DB 2	Length	246			
Best Local Similarity	34.2%	Pred. No.	5.4e-19						
Matches	90	Conservative	42	Mismatches	102	Indels	29	Gaps	7

QY	8	VKGLVAIVTIGSASGLGATLAERLYGQGSANLDDLPNCGE-----AQAKLGNVCV	59
Db	2	LOGKTAIVTIGSSRGIQRATLAEELRHGANVY---NAGNKEKAEKVAAETKEIGAEAI	57
QY	60	FAPADVTESEKIVOTALALAKGKFGRDVPAVACAGIAYASKYINLKGGTHLEDFORVLD	119
Db	58	AIQADVDADSESVQAAVKEITIDTFGAVDILVNNAGITRNLEMRKE-----EDMDAVID	111
QY	120	VNLGTFENVILVAVGEMGQNEPDDGGQR-GVIINTASYAALEGVQGAAYSASKGIYGM	178
Db	112	TNLKGVFHCSSKAVTEPRMVK-----QRFGRIIINSSVYGAIGNAGQANYAAAGVYGL	164
QY	179	TLPIARDLAPIGIRIMTIAEGLFEGPILTLISLEKVCNCLASQVPPSSLDGPAEYAHNY	238
Db	165	TKTLAREELANRNITVYNAAPGIEITDMGELLPEDKAKQMLQIIPV-AALGQPEEYAKAVR	223

```

QY      239 AIIEN--PELNGEYIRLDGAIRM 259
          :  :  :  :  :  :  :  :  :
Db      224 FLASDDASYLTIGQTIHWNGMYM 246

RESULT 17
HR4136
3-oxoacyl-(acyl-carrier protein) reductase BH3896 [imported] - Bacillus halodurans (strain C-1)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

```

R.Takami, H.; Takasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, E.; Hiraoka, Y.; Nakamura, T. *Nucleic Acids Res.* 28, 4317-4331, 2000  
 Article: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
 A:Reference number: AB650; MUID:20512582; PMID:11058132  
 A:Accession: H84136  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-246 <STD>  
 A:Cross-references: GB:AP001520; GB:BA000004; NID:510176401; PIDN:BA07615.1; GSPDB:GN00  
 A:Experimental source: strain C-125

C/gene: BH3896  
C/gene: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
C/superfamily:

Query Match	25.4%;	Score 332;	DB 2;	Length 246;
Best Local Similarity	34.2%;	Pred. No. 7.1e-19;		
Matches 91; Conservative	40;	Mismatches 95;	Indels 40;	Gaps 8;

```

QY      8 KKGVAITIGGASLSIGIATAEPLVGGGASAVLLD-----LPNSGGFAQAKKIG 55
D      3 LINGVAATIGGAGRIGIGAIKAFREBSAKTIVCDVREEEYAKVAIYELODGGGA-----LG 58
QY      56 NNCVFAPADYTSKEDVOTALALAKGKEGRVDVAVNCAGIAVASKTYLNKKGQHTILEDQ 115
D      59 -----SVAYDQORDRDKVNIQVIEREETLDVVVNNAGITADQLTMTDAQ-----WD 107
QY      116 RYLDVNMAGFENVRLTAGEMGQNEPQGGORGVIINTASVAFEGOVGOAAASAKGKI 175
D      108 DVIDVNLKGFVITYQEVTTIKKEQ-----KRGVITLASSVSYSGNEGQTNNAKMGV 161
QY      176 VGMFLPIARDLAPIGIRVMTIAPGLFSTPLLTSLPERVCNFIASSQVFPBSRLDDPAE--- 232
D      162 NGMKRTAKKEIGRINIRVNNAVAPGFIITPMT EKMPKRYLVKMEKKAVL- NRTGTVEEVAN 220
QY      233 -YAHVQAIIENPFLNGEVRIDGAI 257
D      221 GYAFI-ASDPASTITGTIIAIDGV 244

```

## RESULT 18

3oxoacyl-(acyl-carrier-protein) reductase WC021 [imported] - *Vibrio cholerae* (strain 3000)  
C:Species: *Vibrio cholerae*  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C:Accession: F82128  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.; Charbon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoli, I.; Sellers, J. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

A:Reference number: A82035; MUID:20406833; PMID:1095301  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*-  
Nature 405, 411-463, 2000

A:Accession: F82128  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-248 <HEL>  
A:Cross-references: GB:AF004276; GB:AF003852; NID:9665655; PIDN:AAF95169.1; GSPDB:GN  
A:Experimental source: serogroup O1, strain N16961, biotype El Tor  
C:Genetics:

C;superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match:	25.1%	Score 328.5:	DB 2:	Length 248:
Best Local Similarity	32.0%	Pred. No. 1.4e-18:		
Matches 82; Conservative	54;	Mismatches 103;	Indels 17;	Gaps 5;

[illegible]

00 0 NEEBNAVALVIGS KRUGNAI EDELLER KAN VIGTALIG SEKKYALISU LÖBUNGARVARNALIN 1 00

ÖY 67 SEKKYÖTALALAKGRVDVA NCAGI A VASKITYNLKKÖTHIT LEDEFÖRVLVDYINLMGT 1 22

```
D8      :   :   |       :   :   |       :   :   |
66 NPESIEAVLKAITDEGGVDILVNNAGIIRDNLMPKE-----EWSDMIENLTSLF 11
```

[illegible]

187 APIGIRVMTAPGLFECTPLLTSLPEKVCNPLASQVFPFSPRLCDPAETVAHLVQAITENP-- 244

Db 174 ASKSVTVNIVAPGFETDMTKALNDEQRIATLAQYF-AGRLGDPREIASAV-AFLASPEA 23

QY 245 -FLNGEVIRLDGAIRM 259  
::||:::|:|  
Ph 233 AVTTCETI UNNCMVR 247

22

RESULT 19  
E97919  
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [imported] - Streptococcus  
C:Species: Streptococcus pneumoniae

N:Alternate names: protein B2A19.180

C:Species: Neurospora crassa

C>Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 24-May-2001

C:Accession: T51084

R:Schulte, U.; Algen, V.; Hehlsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, July 2000

A:Reference number: 225286

A:Accession: T51084

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-297 <SOCH>

A:Cross-references: EMBL:AL390092; GSPDB:GN00116; NCSP:B2A19.180

A:Experimental source: BAC clone B2A19; strain OR74A

C:Genetics:

A:Gene: NCSP:B2A19.180

A:Map position: 6

A:Insertion: 218/1; 249/1

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match

Best Local Similarity 25.6%; Score 335.5; DB 2; Length 297;

Matches 97; Conservative 39; Mismatches 103; Indels 67; Gaps 8;

6 RSVGLAVITGGASGLATAEIRLVGCGASAVLIDLPNS-----GGEAQ 50

2 RSLHKKALITGGSGSIGLAIRLVLEGGSVTLKRTSTLQASQSLLSQPLHSPAQ 61

51 AKLGNCCVPADVTSEKVOYAL-ALAKGFRVDVAVNCAGIYAS---KTYLKKG 106

62 QPSDKRVSYHPLNVTSASSMEDLLSNSGGRGVDILINCAGITQRSPLMKT----- 115

107 QTHLEFORVLDMVLMGTENVIRLVAGEGONEP-----DOG----- 145

116 ---STEEVEGLDNLNGLTYLGGKFGVRAALRNRPQOHRVAKADSGAGVEGTEEG 172

146 -----QRCVITNTASVAFEGVGOAAYSAKSGIVGKTLPIADLPIGI 191

173 KGEKGGGVREGVVERVIVNVASLAKQKVGISVAAKAAVNGLTSLAEYGRSGI 232

192 RVMTIARGLFETPLTLTSLPEVCNFIASQVFPFSRLDPAEYAHLYQAIENFPLNGEVI 251

233 RVNVLGVYETDITGLKNP---SLIQIPL-GRFETDEVADALFLIKPNYANNCVL 288

252 RLDCAI 257

289 NLDGGL 294

RESULT 14

AH2042

3-oxoacyl-[acyl-carrier protein] reductase [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AH2042

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriduchi,

Nakazaki, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 203-213, 2001

A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AH2042

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-251 <KUN>

A:Cross-references: GB:BA000019; PIDN:BA073593.1; PID:g17130984; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: fabG

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match

Best Local Similarity 25.6%; Score 334.5; DB 2; Length 251;

Matches 97; Conservative 39; Mismatches 103; Indels 67; Gaps 8;

6 RSVGLAVITGGASGLATAEIRLVGCGASAVLIDLPNS-----GGEAQ 50

2 RSLHKKALITGGSGSIGLAIRLVLEGGSVTLKRTSTLQASQSLLSQPLHSPAQ 61

51 AKLGNCCVPADVTSEKVOYAL-ALAKGFRVDVAVNCAGIYAS---KTYLKKG 106

62 QPSDKRVSYHPLNVTSASSMEDLLSNSGGRGVDILINCAGITQRSPLMKT----- 115

107 QTHLEFORVLDMVLMGTENVIRLVAGEGONEP-----DOG----- 145

116 ---STEEVEGLDNLNGLTYLGGKFGVRAALRNRPQOHRVAKADSGAGVEGTEEG 172

146 -----QRCVITNTASVAFEGVGOAAYSAKSGIVGKTLPIADLPIGI 191

173 KGEKGGGVREGVVERVIVNVASLAKQKVGISVAAKAAVNGLTSLAEYGRSGI 232

192 RVMTIARGLFETPLTLTSLPEVCNFIASQVFPFSRLDPAEYAHLYQAIENFPLNGEVI 251

233 RVNVLGVYETDITGLKNP---SLIQIPL-GRFETDEVADALFLIKPNYANNCVL 288

QY 1 MAACRSYKGLVAVITGGASGLATAEIRLVGCGASA-----VLDDPNSG 47

1 MAILSENIRGVAVITGGASGRIGRAIALLELVNAGATVNVYASSSTADEVVAETIGAG 60

QY 48 EAAKRLGNCCVPADVTSEKVOYALALAKGFRVDVAVNCAGIYASVAKTYNLEKQ 107

61 EAVALK-----ADVSQVEQVDNLNGALIDFKRIDILVNNAGITRPTLLKMP-- 109

QY 108 THLEDFQRLVDVLMGTENVIRLVAGEGONEPDQGGQGVITNTASVAFEGVQQA 167

110 ---EDMQAVIDLNTGLVFLCTRAVSRLMKQ-----RSGRIITNTSVAGOMGNPQAN 159

QY 168 YSASKGIVGMLTPARDLADIGIRVMTIARGLFETPLTSLPEVCNFIASQVFPFSRL 227

160 YSAKAGVIGFTKYAKELASRGILVAVNAPGFTATDTSUKSE---GILQYIPL-GRY 215

QY 228 GDPAEYAHLYQAIENP---FLNGEVIRLDGAIEM 259

216 GQPEIAGVNRFLADPAAAYITGGVFNVDGMYV 250

RESULT 15

S22450

3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor, NADPH-dependent

N:Alternate names: beta-ketoacyl-ACP reductase

C:Species: Cuphea lanceolata

C>Date: 16-Feb-1995 #sequence\_revision 23-Feb-1996 #text\_change 17-Mar-2000

C:Accession: S22450; S19832

R:Klein, B.; Pawlowski, K.; Hoeftcke-Grandpierre, C.; Schell, J.; Teepfer, R.

Mol. Gen. Genet. 233, 122-128, 1992

A>Title: Isolation and characterization of a cDNA from Cuphea lanceolata encoding a b

A:Reference number: S22450; MUID:92293104; PMID:1376402

A:Accession: S22450

A:Molecule type: mRNA

A:Residues: 1-320 <KLE>

A:Cross-references: EMBL:X64566; NID:g18045; PIDN:CAA45866.1; PID:g18046

A:Experimental source: immature embryo

C:Genetics:

A:Gene: CLK127

A:Genome: nuclear

C:Function: EC 1.1.1.100 [validated, MUID:92293104]

A:Pathway: fatty acid biosynthesis

A>Note: Integral part of the fatty acid synthase type II

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: chloroplast; fatty acid biosynthesis; NADP; oxidoreductase

F:1-63/Domain: transit peptide (chloroplast) #status predicted <INP>

F:64-320/Product: 3-oxoacyl-[acyl-carrier-protein] reductase #status predicted <MAT>

F:78-258/Domain: short-chain alcohol dehydrogenase homology <SADR>

F:227/Active site: Tyr #status predicted

Query Match

Best Local Similarity 32.7%; Score 334; DB 2; Length 320;

Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;

2 AAACRSYKGLVAVITGGASGLATAEIRLVGCGASAVLIDLPNSGGEA-----QAKKION 56

69 AGAGGVESVAVITGASNGIGKALISL-GRAGCVLVNVARSSSEAEVSKIEAFEG 127

QY 57 NCVFAPADVTSEKVOYALALAKGFRVDVAVNCAGIYASVAKTYNLEKQCHITLEDPR 116

128 QALTFEGDVSKEDVDAMIKTAVDAGTYDILVNNAGITRPTLLKMKRSQ-----WCE 181

QY 117 VLTVNLMGTENVIRLVAGEGONEPDQGGQGVITNTASVAFEGVQQAASAKSGIV 176

182 VIDNLTVPLCLQAQAKIMMK-----KKGRIINAVSVGLVGNAGANSAKAGVI 235

QY 177 GMTLPIARDIAPIGIRVMTIARGLFETPLTSLPEVCNFIASQVFPFSRLDPAEYAH 236

236 GFTKTVAREVARNINNVAVAPGFISSDMTSKIGDINKIIEITPL-GRYQPEEVAGL 294

QY 237 VQAITFNP---FLNGEVIRLDGAIEM 259

RESULT 10  
 F83098  
 Probable short-chain dehydrogenase PA4389 [Imported] - *Pseudomonas aeruginosa* (strain PA  
 C:Species: *Pseudomonas aeruginosa*  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: F83098  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
 A:Reference number: A82950, MUID:20437337, PMID:10584043  
 A:Accession: F83098  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-252 <Sto>  
 A:Cross-references: GB:AE004854; GB:AE004091; NID:99505606; PIDN:AG07777.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA4389  
 A:Superfamily: rblitol dehydrogenase; short-chain alcohol dehydrogenase homology

```

Query Match      27.1%; Score 355; DB 2; Length 252;
Best Local Similarity 35.1%; Pred. No. 1.1e-20;
Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;

QY      8 VKGLVAVITGASGLGATARLYVGQASAVLLDPN-----SGGEQAARKLG 55
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      3 LKDVYIIITGCGSIGRAMEYLLGKGARLYALVPLNRRLEDAVAACKAGGDARA----- 58
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      56 NNCFAPADVYSEKDVOTALALAKGKFRVDVAVNCAGIAVASKTYLKKQOTH--TLED 113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      59 -----YYCNVADEDEQVTHMAQVASFAGINGLVNNAGIILDGTLTKVKDQGLSKMSIAQ 113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      114 FQRLVDVLMATFNVIIRLYAGEMGQ--NEPQGGQGRGIIINTASVAAEFGVYGAASAS 171
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      114 WOSVIDVNLTVFICTREVAAMTELKYE-----GATVVISSTISR AGMGAGANSAA 165
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      172 KGLIVGMLPTARDIARDIGIRVMTIAPQLFETPLTISLPKVCNFFLASQVFPFSLGDPA 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      166 KAGVADIVVAAKELARIGIRVAGVAPFISTEMTAGKRPALAEKMTAGIPL--KRMGKPV 224
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      232 EYAHLYOAIINPFLINGEVIRLDGAIRM 259
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      225 EIAHSVAIIFENDYITGVNLELDGGRL 252

```

RESULT 11  
 P97338  
 3-ketocacyl carrier protein reductase [imported] - Clostridium acetobutylicum  
 C:Species: Clostridium acetobutylicum  
 C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
 C:Accession: P97338  
 R:Noilling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
 A:Reference number: A96900; MUID:21359325; PMID:21359325  
 A:Accession: P97338  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-249 <KUR>  
 A:Cross-references: GB:AE001437; PIDN:AAK81497.1; PIR:J15026670; GSPDB:GN00168  
 A:Experimental source: Clostridium acetobutylicum ATCC2424  
 C:Genetics:  
 A:Gene: CAC3574  
 C:Superfamily: Ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

```

QY      8 VKLAVIINGGASGLATAAEELVQGASAVILDLDPNNGGEAQ-----AKKIGNNCVFAP 62
D      5 LSKRAVAVTGAGRGGLRALALAKLAAGNLV-VNTRSEAEATQALKIEBELSGKAAYK 63

QY      63 ADVTSEKDVOATALATAKKEGFEVDVAVNCAGIYASKTYNLKKQOTHTLEDFOYEDVNL 122
D      64 ADISKDEDEETIIKKALDEYGTVDLIVNAGITKNDLLRPKE-----EDFOSVIVNL 117

QY      123 MGEFNYIRLVAGMGNNEPDGOGGVIINTASVAFAEFGQGAAYSASKGGIYGMTLP1 182
D      118 KGAFNCKIKHTRSMLEK-----KSGKIINSSVGLGLGNNGOVYNYAAKAGIIGMTKSV 171

QY      183 ARDLAPIGIRVMTIAPGLTGTPLLTSLPEKYCNFLASOVPPPSRLGDPAEYAHLYQAIIE 242
D      172 AKELASRGITVYNAAGIIKSDMTDALTDKQRESIYAAVPL-NKVEGEADVANIYLFAS 230

QY      243 --NPFLNGEYIRLDSAIRM 259
D      231 DLSSTYTGQVINVDDGMYM 249

```

RESULT 12  
H72219  
3-oxoacyl-(acyl carrier protein) reductase - *Thermotoga maritima* (strain MSB8)  
C.Species: *Thermotoga maritima*  
C.Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C.Accession: H72219  
R.Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, J.M.; Marshall, W.; Smith, T.F.; Tarr, P.; White, O.; Adams, M.D.; Garavito, R.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.  
Nature 399, 323-329, 1999  
A.Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome  
A.Reference number: A72200; MUID:9928731c; PMID:10360571  
A.Accession: H72219  
A.Status: Preliminary  
A.Molecule type: DNA  
A.Residues: 1-246 <ARN>  
A.Cross-references: GB:AE001811; GB:AE000512; NID:94982291; FIDN:AMD36790.1; PID:9498  
A.Experimental source: strain MSB8  
C.Genetics:  
A.Gene: TMJ74  
C.Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
F.6-185/Dom1n: short-chain alcohol dehydrogenase homology <AD>  
Query Match 26.1%; Score 341; DB 2; Length 246;  
Best Local Similarity 33.7%; Pred. No. 1.4e-19;  
Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;

[illegible]

Query Match	Score	DB	Length	RESULT
Best Local Similarity	26.2%	343.5	249	13
Best Match	33.2%	Pred. No. 9e-20		T51084
86: Conservative	56	Mismatches	96: Indels	21: Gaps
3-xoxocyl-[acyl-carrier-Protein]-reductase (oar-1) [Imported] - Neurospora crassa				



Db 238 NDYNGEVIRLDDGAIKMP 256

RESULT 7

AG2750

3-hydroxyacyl-CoA dehydrogenase type II Atu1415 [Imported] - Agrobacterium tumefaciens C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002

C:Accession: AG2750

R:Wood, D.W.; Seibald, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClellan, S.; Romero, P.; Zhang, S.

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C56.

A:Reference number: AB2577; PMID:11743193

A:Accession: AG2750

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-257 <KUN>

A:Cross-references: GB:AE008688; PIDN:AL42421.1; PID:G17739833; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

A:Gene: Atu1415

A:Map position: circular chromosome

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 49.0%; Score 642; DB 2; Length 257;

Best Local Similarity 51.7%; Pred. No. 3, 1e-43;

Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

Db 7 SVKGLVAVITGASGLTAERLVGQASAVLLDLPNSGGEAOKKLNCCFAPADVT 66

2 NIEGALVITGASGLTAERLVGQASAVLLDLPNSGGEAOKKLNCCFAPADVT 59

QY 67 SEKDVTALALAKGFGVDVAVACAGAVASKTYNLKGQTHLEFORVLDVNLGTF 126

Db 60 SDADQAAIKVAASAKGRLIVNCAGTGTGRI--LGRSPQGLGFEQVIRYNLIGTF 117

QY 127 NVIRLVAGEMGONEPDG---GGRGVINTASVAEFGQVQAAYSASKGGIVGKTLPI 182

Db 118 NMMRLAAAHMEREDDEQDSRODNGVINTASVAEFGQVQAAYSASKGGIVSLALPA 177

QY 183 ARDLAPGIRVMTAPGLFTPLTSLPEKVCNPLASQVPPSPGLGPAEYAHVQAIIE 242

Db 178 ARELARIRIRVNTAPGFLFTPLTSLPEKVCNPLASQVPPSPGLGPAEYAHVQAIIE 237

QY 243 NPEINGEVIRLDDGAIKMP 261

Db 238 NDYNGEVIRLDDGAIKMP 256

RESULT 8

CG2264

3-hydroxyacyl-CoA dehydrogenase [Imported] - Caulobacter crescentus C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001

C:Accession: CG2264

R:Nierman, M.C.; Feldjulyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolot, n. J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 99, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: AB7249; MUID:21173698; PMID:11259647

A:Accession: CG2264

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-260 <STO>

A:Cross-references: GB:AE005673; NID:q13421233; PIDN:AAK22111.1; GSPDB:GN00148

A:Gene: CC0124

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 45.5%; Score 595; DB 2; Length 260;

Best Local Similarity 51.0%; Pred. No. 1, 6e-39;

Matches 130; Conservative 30; Mismatches 89; Indels 6; Gaps 2;

QY 11 LVAVITGASGLTAERLVGQASAVLLDLPNSGGEAOKKLNCCFAPADVTSEKD 70

Db 7 VAAYVITGASGLTAERLVGQASAVLLDLPNSGGEAOKKLNCCFAPADVTSEKD 64

QY 71 VQTAALALAKGFGVDVAVACAGAVASKTYNLKGQTHLEFORVLDVNLGTF 126

Db 65 VAGEEKAHAHQEILVNCAGTGTGRI--LGRSPQGLGFEQVIRYNLIGTF 124

QY 127 NVIRLVAGEMGONEPDGSGRVIINTASVAEFGQVQAAYSASKGGIVGKTLPIARDL 186

Db 125 RCLASAKGMLDLEPDERGALVNTASVAEFGQVQAAYSASKGGIVGKTLPIARDL 184

QY 187 APGIRVMTAPGLFTPLTSLPEKVCNPLASQVPPSPGLGPAEYAHVQAIIE 246

Db 185 MEGIRVNTILPGIFNTPLMNAPEAVKGLAASVFPKRGHPBEYQALATMTTCGF 244

QY 247 NGEVIRLDDGAIKMP 261

Db 245 NGEVIRLDDGAIKMP 259

RESULT 9

E70740

probable fabG2 protein - Mycobacterium tuberculosis (strain H37RV) C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000

C:Accession: E70740

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajendram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome.

A:Reference number: A70500; MUID:9825987; PMID:9634230

A:Accession: E70740

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-247 <COL>

A:Cross-references: GB:Z75555; GB:AL123456; NID:q3261608; PIDN:CAA99983.1; PID:q14190

A:Experimental source: strain H37RV

A:Gene: fabG2

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

F:8-186/Domain: short-chain alcohol dehydrogenase homology <SABH>

Query Match 29.3%; Score 383.5; DB 2; Length 247;

Best Local Similarity 38.9%; Pred. No. 6, 4e-23;

Matches 96; Conservative 43; Mismatches 91; Indels 17; Gaps 5;

QY 13 AVITGASGLTAERLVGQASAVLLDLPNSGGEAOKKLNCCFAPADVTSEKD 70

Db 10 AVITGASGLTAERLVGQASAVLLDLPNSGGEAOKKLNCCFAPADVTSEKD 69

QY 71 VQTAALALAKGFGVDVAVACAGAVASKTYNLKGQTHLEFORVLDVNLGTF 130

Db 70 VDLIRAVRFRGLDVVNMAGITRDATN-----RTMEEDPDQVIAVHLKGTNGNR 123

QY 131 LVAGEMGONEPDGSGRVIINTASVAEFGQVQAAYSASKGGIVGKTLPIARDLAPG 190

Db 124 LAALAIKER-----KRGALVNMSSVSGKVMGQNTYSAKAGVIGMKAARELAHNG 177

QY 191 IRVMTAPGLFTPLTSLPEKVCNPLASQVPPSPGLGPAEYAHVQAIIE--NPEFLNG 248

Db 178 IRVMTAPGLFTPLTSLPEKVCNPLASQVPPSPGLGPAEYAHVQAIIE--NPEFLNG 248

QY 249 EVIRLDDG 255

Db 237 TVLDVVG 243

Probable dehydrogenase - Mycobacterium tuberculosis (strain H37Rv)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: A70554  
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellern, S.; Squares, S. Nature 393: 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9654230  
A:Accession: A70554  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-250 <COL>  
A:Cross-References: GB:A55584; GB:AL123456; NID:g3261774; PIDN:CAB09032.1; PID:g2117182  
A:Experimental source: Strain H37Rv  
C:Genetics:  
A:Gene: Rv1144  
A:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
F:6-187/Domain: short-chain alcohol dehydrogenase homology <SAD>  
Query Match 51.3%; Score 671.5; DB 2; Length 250;  
Best Local Similarity 60.1%; Pred. No. 1.4e-45;  
Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;  
QY 9 KGLVAVITGASGGLATAEERLVGASAVLLDLPNSGGEQAQKLGNNCFAPADYTS 68  
DB 4 KDAVAVVVGASGGLATKRLDAGAVVVDL---RGDDVVGGLDRARFAQADYTD 60  
QY 69 KDVCATLALAKGKGRVDVAVNCGIAVASKTYNKKQHTLEDFOVLVDVNLMTGFN 128  
DB 61 AAVSNALFLA-DSLGPNVAVVNCAGTGNALRV--LSRQVFPPLAEFRKYDINLVGFNV 117  
QY 129 IRLVAVGEMQNEPDGQGRVITNTASVAFAEGVQGAASAKSGIVGMLPIARLAP 188  
DB 118 IRLGFERIAKTEP-IGSERGVITNTASVAFAEGVQGAASAKSGIVGMLPIARLAP 176  
QY 189 IGRVMTAPGLFGTPLTSLPEKVCNPLASQVPPSRGLDPAEYAHVQAIIENPFLNG 248  
DB 177 KLIRVVTAPGLFGTPLTSLPEKVCNPLASQVPPSRGLDPAEYAHVQAIIENPFLNG 236  
QY 249 EVIRLDGAIKMQP 261  
DB 237 EVIRLDGAIKMQP 249

Probable dehydrogenase - Mycobacterium tuberculosis (strain H37Rv)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: A70554  
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellern, S.; Squares, S. Nature 393: 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9654230  
A:Accession: A70554  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-250 <COL>  
A:Cross-References: GB:A55584; GB:AL123456; NID:g3261774; PIDN:CAB09032.1; PID:g2117182  
A:Experimental source: Strain H37Rv  
C:Genetics:  
A:Gene: Rv1144  
A:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
F:6-187/Domain: short-chain alcohol dehydrogenase homology <SAD>  
Query Match 51.3%; Score 671.5; DB 2; Length 250;  
Best Local Similarity 60.1%; Pred. No. 1.4e-45;  
Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;  
QY 9 KGLVAVITGASGGLATAEERLVGASAVLLDLPNSGGEQAQKLGNNCFAPADYTS 68  
DB 4 KDAVAVVVGASGGLATKRLDAGAVVVDL---RGDDVVGGLDRARFAQADYTD 60  
QY 69 KDVCATLALAKGKGRVDVAVNCGIAVASKTYNKKQHTLEDFOVLVDVNLMTGFN 128  
DB 61 AAVSNALFLA-DSLGPNVAVVNCAGTGNALRV--LSRQVFPPLAEFRKYDINLVGFNV 117  
QY 129 IRLVAVGEMQNEPDGQGRVITNTASVAFAEGVQGAASAKSGIVGMLPIARLAP 188  
DB 118 IRLGFERIAKTEP-IGSERGVITNTASVAFAEGVQGAASAKSGIVGMLPIARLAP 176  
QY 189 IGRVMTAPGLFGTPLTSLPEKVCNPLASQVPPSRGLDPAEYAHVQAIIENPFLNG 248  
DB 177 KLIRVVTAPGLFGTPLTSLPEKVCNPLASQVPPSRGLDPAEYAHVQAIIENPFLNG 236  
QY 249 EVIRLDGAIKMQP 261  
DB 237 EVIRLDGAIKMQP 249

RESULT 6  
F97531  
Probable short-chain dehydrogenase (PA2554) [Imported] - Agrobacterium tumefaciens (S)  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
C:Accession: F97531  
R:Goodner, B.; Hinkle, G.; Gattling, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldm, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium  
A:Reference number: A97559; PMID:11743194  
A:Accession: F97531  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-257 <KUR>  
A:Cross-References: GB:AE007869; PIDN:AAK87207.1; PID:g15156487; GSPDB:GND0169  
C:Genetics:  
A:Gene: AGR\_C\_2613  
A:Map position: circular chromosome  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
Query Match 49.0%; Score 642; DB 2; Length 257;  
Best Local Similarity 51.7%; Pred. No. 3.1e-43;  
Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;  
QY 7 SVKGLVAVITGASGGLATAEERLVGASAVLLDLPNSGGEQAQKLGNNCFAPADYTS 66  
DB 2 NIEGAGALVTCAGSAGLCAVAARMILARGAATVTFDRNGEAGKRLAAEIGKAV--OGDVA 59  
QY 67 SEKDVQATLALAKGKGRVDVAVNCGIAVASKTYNKKQHTLEDFOVLVDVNLMTGFN 126  
DB 60 SDDAQCAIRVVAASAKGGLIIVNCGETGACRI--LGRGPOPLDPEVIRYNLIGTF 117  
QY 127 NVIRLVAVGEMQNEPDG---GQGVITNTASVAFAEGVQGAASAKSGIVGMLTPI 182  
DB 118 NNMRLAAHMAERRODEGQOSRODNGVITNTASVAFAEGVQGAASAKSGIVSLTLP 177  
QY 183 ARDLAPGIRVMTAPGLFGTPLTSLPEKVCNPLASQVPPSRGLDPAEYAHVQAII 242  
DB 178 ARELARIRVNTVAPGIFLPLDGLPQEVQSLAGQIIPSRGLDPAEYAHVQAII 237  
QY 243 NPLNGEVIRLDGAIKMQP 261

## ALIGNMENTS

RESULT 1  
T20484  
hypothetical protein F01G4.2 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T20484  
R.Harris, B.  
submitted to the EMBL Data Library, January 1996  
A:Reference number: 219281  
A:Accession: T20484  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-258 <M1>  
A:Cross-references: EMBL:268341; PIDN:CAA92764.1; GSPDB:GN00022; CESP:F01G4.2  
A:Experimental source: Clone F01G4  
C:Genetics:  
A:Gene: CESP:F01G4.2  
A:Map position: 4  
A:Intons: 8/3; 61/3; 116/3; 162/3; 209/3  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 57.1%; Score 748; DB 2; Length 258;  
Best Local Similarity 59.9%; Pred. No. 1.4e-51;

Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;

QY 3 AACRSYGLVAVITGASGLGLATPERLYVGOGASAVLDDLPNSGGEAQAQKLGNNCVAP 62  
DB 2 SALRSKGLVAVITGASGLGKGALEVLAKAGVAILDLPQSKADYAKETGG--ITFP 59  
QY 63 ADVTSEKDVQALALAKGKFGNVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDVNL 122  
DB 60 ASVTSEEEVRAFAKVAQAEYGRDLVNCAGIYAFKLYSVQKKHVDPEKIRQTIQVNV 119  
QY 123 MGFENYRLVAGMGQNEPDGQGRVINTASVAFAEGOVQAAYASAKSGIVMTLPI 182  
DB 120 LGFNVIRRGVALMGHEKNDANGQKGVINTASVAFAFDQGTQGSVSKGAIYMTLPI 179  
QY 183 ARDLAIGIRVMTIAPGLGTPLTSLPEKVCNFIASQVPPPSRLGDPAEVYHLVQAIIE 242  
DB 180 ARPFADGIRFNFIAPGLMDTPLSLPEKVSFLAQLIPNSRLGHPHEYGLVQHIIE 239  
QY 243 NPFLNGEVIRLDGAI RM 259  
DB 240 NCYLNGETIRFDGAL RM 256

RESULT 2  
H83326  
probable short-chain dehydrogenase PA2554 [imported] - *Pseudomonas aeruginosa* (strain PA  
C:Species: *Pseudomonas aeruginosa*  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: H83326  
R.Stover, C.K.; Pham, X.Q.; Ewin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Bz  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, J.; Linn,  
J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
A:Reference number: A82950; M01D:20437337; PMID:10984043  
A:Accession: H83326  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-255 <STO>  
A:Cross-references: GB:AE004683; GB:AE004091; NID:g9948607; PIDN:AAG05942.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA2554  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 55.0%; Score 720; DB 2; Length 255;  
Best Local Similarity 57.5%; Pred. No. 2.3e-49;

Matches 145; Conservative 39; Mismatches 66; Indels 2; Gaps 1;

QY 8 VKGLVAVITGASGLGLATPERLYVGOGASAVLDDLPNSGGEAQAQKLGNNCVAPADYTS 67  
DB 3 IENRVFLITGASGLGAATAKMLVEQGVYLVADINAEAGAKAAELGQAFVRADLNS 62  
QY 68 EKDVTALALAKGKFGNVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDVNLGTFN 127  
DB 63 EADGRQAVAAALAFGLHGLACAGVAPAEKV--LGRNIGHALESFRRVIDINLVGSEFN 120  
QY 128 VIRLVAGMGQNEPDGQGRVINTASVAFAEGOVQAAYASAKSGIVMTLPIARDLA 187  
DB 121 MLRLAAEAMSGQPDDEGGERGVINTASVAFAFDQGTQGSVSKGAIYMTLPIARELA 180  
QY 188 PIGIRVMTIAPGLGTPLTSLPEKVCNFIASQVPPPSRLGDPAEVYHLVQAIIEPNFLN 247  
DB 181 RFGIRVMTIAPGLGTPLTSLPEKVCNFIASQVPPPSRLGDPAEVYHLVQAIIEPNFLN 240  
QY 248 GEVIRLDGAI RM 259  
DB 241 GEVIRLDGAI RM 252

## RESULT 3

AG3611  
3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100) [imported] - *Brucella melitt*  
C:Species: *Brucella melittensis*  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 15-Feb-2002  
C:Accession: AG3611  
R.DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov  
J.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitt*  
A:Reference number: AD3252; PMID:11736688  
A:Accession: AG3611  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-255 <KUP>  
A:Cross-references: GB:AE008918; PIDN:AAL54058.1; PID:g17985013; GSPDB:GN00191  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BME110816  
A:Map position: 11  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
C:Keywords: oxidoreductase

Query Match 54.3%; Score 711; DB 2; Length 255;  
Best Local Similarity 57.1%; Pred. No. 1.2e-48;  
Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

QY 8 VKGLVAVITGASGLGLATPERLYVGOGASAVLDDLPNSGGEAQAQKLGNNCVAPADYTS 67  
DB 3 IENRVFLITGASGLGAATAKMLVEQGVYLVADINAEAGAKAAELGQAFVRADLNS 62  
QY 68 EKDVTALALAKGKFGNVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDVNLGTFN 127  
DB 63 DTDGKAALAALEAFSRDLYVNCAGVAPAEKV--LGRGAKHKEETTRTISINLITFN 120  
QY 128 VIRLVAGMGQNEPDGQGRVINTASVAFAEGOVQAAYASAKSGIVMTLPIARDLA 187  
DB 121 MLRLAAEAMSGQPDDEGGERGVINTASVAFAFDQGTQGSVSKGAIYMTLPIARELA 180  
QY 188 PIGIRVMTIAPGLGTPLTSLPEKVCNFIASQVPPPSRLGDPAEVYHLVQAIIEPNFLN 247  
DB 181 RFGIRVMTIAPGLGTPLTSLPEKVCNFIASQVPPPSRLGDPAEVYHLVQAIIEPNFLN 240  
QY 248 GEVIRLDGAI RM 259  
DB 241 GEVIRLDGAI RM 252

## RESULT 4

AT0534





Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

QY 12 VAVITGASGLATAEERLVGOGASAVILLDLPSNGSGE---AQAALGNCCVAPADYVS 67  
 DB 5 IAVYTGMSGIGTALICORLAKDFRVAAGCGSPSPREKLEQOKALGDFIASEGNVAD 64  
 QY 68 EKDVOITALAKGKEGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFQRYLVNLMGTN 127  
 DB 65 WDSKTFAPDKYKSEVGEVDVLLNNAGI---TRDYVERK---MTRADWDVADITNLSLFP 118  
 QY 128 VIRVAGBMQNEEDDGGGQGVIIINTFASVAFEGOVGOAAYSASKGIYGMTIPIRADA 187  
 DB 119 VTKOYIIGMA---DRWM---GRIVNISVNGOKGQEGCTYNTAKAGLHFTMALAQEVA 172  
 QY 188 PIGIRVMTIAPGLTGLTSLPEKYCNFLASOVPEPSRLGDPAEYAHVQAII--ENPF 245  
 DB 173 TKGTAVNTVSPGYIATDMVKAIRQDVLDKIATIPV-KRLGLEBELIASICAWLSSESGF 231  
 QY 246 LNGEVIRLDGAIRM 259  
 DB 232 STGADFSILNGGLHM 245

## RESULT 24

PHAB\_ACISP STANDARD; PRT: 248 AA.  
 AC P50203: 01-NOV-1997 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Acetoacetyl-CoA reductase (EC 1.1.1.36).  
 GN PHAB.  
 OS Acinetobacter sp. (strain RA3849).  
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;  
 OC Acinetobacter.  
 NCBI\_TaxID=472;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95362679; PubMed=7635832;  
 RA Schombert M.A., Bayly R.C., Davies J.K.;  
 RT "Phosphate concentration regulates transcription of the Acinetobacter  
 polyhydroxyalkanoic acid biosynthetic genes";  
 RL J. Bacteriol. 177:4501-4507(1995).  
 CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-CoA + NADPH.  
 CC -1- PATHWAY: Polyhydroxyalkanoic acid biosynthesis; second step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SCR) FAMILY.  
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CC EMBL: U37761; AAA9472.1; -  
 CC DR HSSP: P19992; IHDC.  
 CC DR InterPro: IPR002198; ADH\_short.  
 CC DR Pfam: PF00106; adh\_short; 1.  
 CC DR PRINTS: PR00080; SDRFAMILY.  
 CC DR PROSITE: PS00061; ADH\_SHORT; 1.  
 CC KW Oxidoreductase; NADP.  
 CC FT NP\_BIND 9 33 NADP (BY SIMILARITY).  
 CC FT ACT\_SITE 155 155 BY SIMILARITY.  
 CC SQ SEQUENCE 248 AA: 26727 MW: 850E0DC659795123 CRC64;

Query Match 21.8%; Score 286; DB 1; Length 248;  
 Best Local Similarity 31.5%; Pred. No. 2,2e-15;  
 Matches 81; Conservative 47; Mismatches 105; Indels 24; Gaps 7;

QY 12 VAVITGASGLATAEERLVGOGASAVILLDLPSNGSGE-----LGNCCVAPAD 64  
 DB 6 VALVTGALGGIGSEICRQLVTAGYKIITVPRE--EDREKQWLQSEGFQSDVRFVLT 63  
 QY 65 VSEKDVOITALAKGKEGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFQRYLVNLMG 124  
 DB 64 LNNHRAAIALIOEALAAEGRDVLYNNAGI---TRDAIFK---MSYQMGQVIDTINKT 117  
 QY 125 TENVIRLVAGENGQNEPDGGQGVIIINTFASVAFEGOVGOAAYSASKGIYGMTLPIAR 184  
 DB 118 LEFTVQPVFNKMLEO-----KSGRIVNISSVNGLKGQFGOGAANYASAKGIIGFTKALQ 171  
 QY 185 DLAPIGIRVMTIAPGLTGLTSLPEKYCNFLASOVPEPSRLGDPAEYAHVQAII--E 242  
 DB 172 EGARSNTCVNVVAPGRTATPVTAKREDYIKSIEQIFL-QRLAAPALIAAVMTIVSEH 230  
 QY 243 NPELVGEVIRLDGAIRM 259  
 DB 231 GAVTGETLSINGGLYM 247

## RESULT 25

Y019\_THEMEA STANDARD; PRT: 256 AA.  
 AC O56318: 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative oxidoreductase TM0019 (EC 1.-.-.-).  
 GN TM0019.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogae; Thermotogales;  
 OC Thermotogaceae; Thermotoga.  
 NCBI\_TaxID=2336;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MSB8 / DSM 3109;  
 RX MEDLINE=96125254; PubMed=8550425;  
 RA Kletzin A., Adams M.;  
 RT "Molecular and phylogenetic characterization of pyruvate and 2-ketoglutarate ferredoxin oxidoreductases from Pyrococcus furiosus and pyruvate ferredoxin oxidoreductase from Thermotoga maritima";  
 RL J. Bacteriol. 178:248-257(1996).  
 CC [2]  
 CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-CoA + NADPH.  
 CC -1- PATHWAY: Polyhydroxyalkanoic acid biosynthesis; second step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SCR) FAMILY.  
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CC EMBL: X85171; CAAS9459.1; -  
 CC DR EMBL: AE001690; MAD35113.1; -  
 CC DR HSSP: O70351; IE6W.  
 CC DR TIGR: TM0019; -  
 CC DR InterPro: IPR002198; ADH\_short.  
 CC DR Pfam: PF00106; adh\_short; 1.

DT 01-OCT-1994 (Rel. 30, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Oxidoreductase ucpa (EC 1.1.1.177).  
 GN ucpa OR SPM2445 OR STY2682.  
 OS Salmonella typhimurium, and  
 OS Salmonella typhimurium.  
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 OC NCBI\_TaxID=602, 601,  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21534948; PubMed=11677609; / SGC1412 / ATCC 700720;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., All J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 RT LT2".  
 RL Nature 413:852-856(2001).  
 RN [2]  
 RP SEQUENCE OF 204-263 FROM N.A.  
 RC SPECIES=S.typhimurium;  
 RX MEDLINE=91358382; PubMed=1909324;  
 RA Hyrliewicz M.M., Kredich N.M.;  
 RT "The cysP promoter of Salmonella typhimurium: characterization of two  
 RT binding sites for CysB protein, studies of in vivo transcription  
 RT initiation, and demonstration of the anti-inducer effects of  
 RT thiosulfate".  
 RL J. Bacteriol. 173:5876-5886(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.typhi; STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaiha M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrett B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18".  
 RL Nature 413:848-852(2001).  
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDS) FAMILY.  
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Query Match 22.0%; Score 288; DB 1; Length 263;  
 Best Local Similarity 32.2%; Pred. No. 1,7e-15;  
 Matches 85; Conservative 38; Mismatches 105; Indels 36; Gaps 8;

QY 10 GLVAVITGASGIGLATARLVGOGASAVLLDLPNSGGEAOKKL-----GNCCVAP 62  
 Db 6 GTALITGASOGIGIEIARVFARHGANLILLIDISD-----ETEKLADELGRGHRCIVK 60  
 QY 63 ADVTSERKQOTALALAKKRGFRVAVNCGIATAVASKTYNLKGGQHTLEDFQVLDVNL 122  
 Db 61 ADVDRASVQAAVARKKTEGRIDILVNVAGVCRGNFLDMSE-----EDDFRIDINI 114  
 QY 123 MGTENVIRLVAGMGQNEPDGQRCVITINTASVAA-FEGVQQAAYSASKGVGMPLP 181  
 Db 115 KGVAVNTKAVLPENIRKD-----GRIVAMSSVTGDMVADPGETAVALSKAIVGLTKS 168  
 QY 182 IARDLAPIGIRVMTIAPGLFGPPLTSL-----PEKCNPLASQVFPRLGDPAY 233  
 Db 169 LAEVIQSGIRVATCPGVYRTPMARSIAQSNPDDESVLTAKATPL-RLIADPLEV 227  
 QY 234 AELVQ--ATLENPLNGEVRIDG 255  
 Db 228 GELAAFLASDESSYINGTQNVIDG 251  
 RESULT 23  
 PHBB\_ALCEU STANDARD; PRT; 246 AA.  
 ID PHBB\_ALCEU  
 AC P14697;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Acetoacetyl-CoA reductase (EC 1.1.1.36).  
 GN PHBB.  
 OS Alcaligenes eutrophus (Ralstonia eutropha).  
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;  
 OC Ralstonia.  
 OC NCBI\_TaxID=510;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H16 / DSM 428 / ATCC 17699;  
 RX MEDLINE=89359356; PubMed=2670935;  
 RA Peoples O.P., Sinskey A.J.;  
 RT "Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus H16.  
 RT Characterization of the genes encoding beta-ketothiolase and  
 RT acetoacetyl-CoA reductase".  
 RL J. Biol. Chem. 264:15293-15297(1989).  
 RL -1 CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-  
 RL CoA + NADPH.  
 CC -1 PATHWAY: Poly-beta-hydroxybutyrate biosynthesis; second step.  
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
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Query Match 22.0%; Score 287.5; DB 1; Length 246;  
 Best Local Similarity 31.9%; Pred. No. 1,7e-15;



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CC -----  
DR EMBL; AE000752; AAC07575.1; -  
DR HSSP; P50163; 2AE1.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short.1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.  
FT NP\_BIND 12 NADP (BY SIMILARITY).  
FT ACT\_SITE 157 157 BY SIMILARITY.  
SQ SEQUENCE 248 AA; 26867 MW; 5CFDEB9AD83F2C5 CRC64;

Query Match 22.2%; Score 290.5; DB 1; Length 248;  
Best Local Similarity 30.0%; Pred. No. 1e-15; Mismatches 109; Indels 21; Gaps 6;  
Matches 77; Conservative 50; Mismatches 109; Indels 21; Gaps 6;

QY 8 VKGLVAVITGSGASGLIATARLVGOGASAVLLDLPNSGGEAOKKIGN---NCVFAPA 63  
DB 5 LOGVSLVITGSTRIGRAIAEKLASAGSVITITGSGERAKAAVEETANKYGVKAGVEM 64  
QY 64 DYTEKDVOTLALAKKFGKVDVAVNCAGIAVASKTYNKKGGTHLEDFORLVNLM 123  
DB 65 NLISEESTNKAFEEITVLDGIDLVNNAAGITTRDKFLRM-----SLDMEVLYKNLT 118  
QY 124 GTFVYIRLVAGMGONPEPDGGR-GYIINTASVAFAEGVGQAAYSASKGIVGMTLP 182  
DB 119 GTFVLTQNSLRKMK-----QWGRIVNISVVGFTGVNAGVYSTFRAGLIGFETKSL 171  
QY 183 ARDLAPIRVMTIAPGLFGTFLTLSPKXCNFLASGPPPSRLGDPAEVAMHYQATIE 242  
DB 172 AKELAPRVNLVNAVAPGFIETDMTRAVLSEETKQYKEQIPL-GRFSPSEVANYVFLCS 230  
QY 243 N-PFUNGCVIRLDGAI 257  
DB 231 ELASVITGEVIVHNGM 247

RESULT 21  
FABG\_ECOLI STANDARD; PRT; 244 AA.  
ID P25716; P78221;  
AC 01-MAY-1992 (Rel. 22, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 3-oxoacyl-[acyl-carrier protein] reductase (Ec 1.1.1.100) (3-ketoacyl-  
DE acyl carrier protein reductase).  
GN FABG OR B1093.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_Taxid=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE-92210530; PubMed-1556094;  
RA Rawlings M., Cronan J.E. Jr.;  
RA "The gene encoding Escherichia coli acyl carrier protein lies within  
RA a cluster of fatty acid biosynthetic genes.";  
RL J. Biol. Chem. 267:5751-5754(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE-97426617; PubMed-9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.,  
RT "The complete genome sequence of Escherichia coli K-12."

RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE-97061202; PubMed-8905232;  
RA Oshima T., Alpha H., Baba T., Fujita K., Hayashi K., Honjo A.,  
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
RA Yano M., Horiuchi T.;  
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 12.7-28.0 min region on the linkage map.";  
RL DNA Res. 3:137-155(1996).  
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
CC PATHWAY.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY.  
CC -----  
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CC -----  
DR EMBL; M84991; AAA3739.1; -  
DR EMBL; AE000210; AAC74177.1; -  
DR EMBL; D90745; BAA35901.1; -  
DR PIR; B42147; B42147.  
DR HSSP; P29132; 1DFT.  
DR Ecogene; EG11318; fabG.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short.1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.  
FT NP\_BIND 10 NADP (BY SIMILARITY).  
FT ACT\_SITE 151 151 BY SIMILARITY.  
FT CONFLICT 30 30 A -> G (IN REF. 1).  
FT CONFLICT 30 30 A -> G (IN REF. 1).  
SQ SEQUENCE 244 AA; 25560 MW; 48EC1F2A7FEEDF9 CRC64;

Query Match 22.1%; Score 289.5; DB 1; Length 244;  
Best Local Similarity 30.0%; Pred. No. 1.2e-15; Mismatches 112; Indels 15; Gaps 4;  
Matches 76; Conservative 50; Mismatches 112; Indels 15; Gaps 4;

QY 9 KGLVAVITGSGASGLIATARLVGOGASAVLLDLPNSGGEAOKKIGNCVAPADVISE 68  
DB 4 EGRALVTGASRGIRIAETLAARGAKVIGATISNGAALISDYLGANGKGLMNVDP 63  
QY 69 KDVTALALAKKFGKRDVAVNCAGIAVASKTYNKKGGTHLEDFORLVNLMSTENV 128  
DB 64 ASIESVLEKTRAEFGEVDLVNNAAGITTRDLKRMKD-----EENNDIETNLSVFL 117  
QY 129 IRLVAGMGONPEPDGGRGVIIINTASVAFAEGVGQAAYSASKGIVGNTLPIDRLAP 188  
DB 118 SKAYMRMRMK-----RHRITITGSGVETMGNGGANYAAKAGLIGFSKSLAREVAS 171  
QY 189 IGRVMTIAPGLFGTFLTLSPKXCNFLASQVPPPSRLGDPAEVAMHYQATIE 246  
DB 172 RGIIVNVVAPGFIETDMTRALSDORAGIIAQPV-AGRIGAGQEIANAFAVFLASDEAYI 230  
QY 247 NGEVIRLDGAI 259  
DB 231 TGETLVHNGM 243

RESULT 22  
UCPA\_SALTY STANDARD; PRT; 263 AA.  
ID UCPA\_SALTY  
AC 237441.

DR PIR: A28212; A28212.  
 DR PIR: A26938; A26938.  
 DR PIR: B37762; B37762.  
 DR HSSP: P19992; 1HDC.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Oxidoreductase; NAD; Bile acid catabolism; Multigene family.  
 KM NP\_BIND 7 13 NAD (POTENTIAL).  
 FT NP\_BIND 32 36 NAD (POTENTIAL).  
 FT ACT\_SITE 157 157 TSKA -> YOGG (IN REF. 2).  
 FT CONFLICT 159 162  
 SQ SEQUENCE 249 AA; 26658 MW; 084E380921D72C93 CRC64;

Query Match 22.3%; Score 292; DB 1; Length 249;  
 Best Local Similarity 30.7%; Pred. No. 7.7e-16;  
 Matches 83; Conservative 45; Mismatches 98; Indels 44; Gaps 10;

DB 8 VKGLVAVITGGASGLIATAEELVGGASAVLLDLPNSGGE-----AQAKK----- 53  
 4 VODKTIITGSTRIGFAAAKLFTEINGAKVSIF-----GTOEEVDALAQLELYPEE 57  
 QY 54 --LGNVCFADVYSEKDVQATALAKKFRGVAVNCAGIYVASKTYNLKKGQHTL 111  
 DB 58 EVLG---FAP-DLTSRDVAAAGVYAAQKIGRLDVMINNAGITMNSVFSRVSF----- 106  
 QY 112 EDFQRLDVNLMGTFFNIRLVAGMGONEPDGGQGVYINTASVAAFEQGVGQAAYSAS 171  
 DB 107 EDFKINDINNVGFN-----GAMSAVQCKMKAQGVYIINTASVTGLYGLSGISGYPIS 160  
 QY 172 KGVIGMTLPARLAPLIGIRVMTIAPGLFTPLTSLPEVCNVLASQVFFPRLDPA 231  
 DB 161 KAGVIGLHGLGRELIRNRVGVAPGVDPDITMKGPLLEDYLTLPK-KRMKPE 219  
 QY 232 EYAHVQAIIENPFLNG---EVIRLDGAIR 258  
 DB 220 EIAN-VYLFASDLASGITATTISVDGAYR 248

## RESULT 19

FABG\_VIBHA  
 ID FABG\_VIBHA STANDARD: PRT; 244 AA.

AC P55336;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).  
 DE FABG.  
 GN Vibrio harveyi.  
 OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibriio.  
 OC NCBI\_Taxid=665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B392;  
 RX MEDLINE=96134997; PubMed=8550484;  
 RA Shen Z., Byers D.M.;  
 RT "Isolation of Vibriio harveyi acyl carrier protein and the fabg, acpp, and fabp genes involved in fatty acid biosynthesis.";  
 RL J. Bacteriol. 178:571-573(1996).  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS PATHWAY.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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DR EMBL: U39441; AAC43589.1;  
 DR HSSP: P19992; 1HDC.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 KM Fatty acid biosynthesis; Oxidoreductase; NADP.  
 FT NP\_BIND 10 34 NADP (BY SIMILARITY).  
 FT ACT\_SITE 151 151 BY SIMILARITY.  
 SQ SEQUENCE 244 AA; 25519 MW; FC41ALC586CDAAA CRC64;

Query Match 22.3%; Score 291.5; DB 1; Length 244;  
 Best Local Similarity 29.8%; Pred. No. 8.3e-16;  
 Matches 76; Conservative 51; Mismatches 113; Indels 15; Gaps 4;

QY 7 SVKGLVAVITGGASGLIATAEELVGGASAVLLDLPNSGGEAAKKGKGNVCFADVY 66  
 DB 2 NIEGKIALVYVAGSRGIGRAIAELVGVAVIGTATSEGAALISYLENGKGLALANT 61  
 QY 67 SEKDVOITALAKKFRGVAVNCAGIYVASKTYNLKKGQHTLEDQFQVLDVNLMTG 126  
 DB 62 DVESEIATLTKTINDECGAIDILVNNAGITRDNLMMKRD-----DEMNDIINTNLTPIY 115  
 QY 127 NVIRLVAGMGONEPDGGQGVYINTASVAAFEQGVGQAAYSASKGVIGMTLPARL 186  
 DB 116 RMSKAVLRGMMK-----FAGRIIVSGVGTMGAGQNTNAAAGVIGTKSKAREY 169  
 QY 187 APIGRVMTIAPLFTPLTSLPEVCNVLASQVFFPRLDPAEYAHLY--QALITNP 244  
 DB 170 ASRGVYVNTYVAPFIEIDMTKALNDGQRAATLSNV-AGRLGDFRIFASAVYFLASPEAA 228  
 QY 245 FLNGEVIRLDGAIRM 259  
 DB 229 YITGETLHVNGGYM 243

## RESULT 20

FABG\_AQUAE  
 ID FABG\_AQUAE STANDARD: PRT; 248 AA.

AC O67610;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).  
 DE FABG OR AQ\_1116.  
 GN Aquifex aeolicus.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;  
 CC Aquifex.  
 OC NCBI\_Taxid=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=V55;  
 RX MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";  
 RL Nature 392:353-358(1998).  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS PATHWAY.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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QY 243 NPLFNGEVRIDG 255  
Db 229 SSVYTGAEIADVG 241

RESULT 17  
Y4VL\_RHISN  
ID Y4VL\_RHISN STANDARD; PRT; 548 AA.

AC Q53217;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 01-NOV-1997 (Rel. 35, Last annotation update)  
GN Putative short-chain type dehydrogenase/reductase Y4VI (EC 1.-.-.-).  
Y4VI.  
OS Rhizobium sp. (strain NGR234).  
OC Plasmid sym PNG8234a.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
CC Rhizobiaceae; Rhizobium.  
OX NCBI\_taxid=394;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97305956; PubMed=9163424;  
RA Freilberg C.A., Pella R., Bairoch A., Broughton W.J., Rosenthal A.,  
RT Perret X.;  
RL "Molecular basis of symbiosis between Rhizobium and legumes";  
RL Nature 387:394-401(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96389014; PubMed=8796346;  
RA Freilberg C., Perret X., Broughton W.J., Rosenthal A.;  
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.  
RT NGR234 using dye terminators and a thermostable 'sequenase': a  
RT beginning";  
RL Genome Res. 6:590-600(1996).  
RN [1]  
RT -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY. CONTAINS TWO DOMAINS.  
CC  
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CC  
CC EMBL: 268203; CA92424.1; ALT\_INT.  
DR EMBL: AE00101; AAB91897.1; -.  
DR HSP; P50163; ZAE1.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short; 2.  
DR PROSITE: PS00061; ADH\_Short; 1.  
KW Hypothetical protein; Oxidoreductase; Plasmid; Repeat;  
KW Multifunctional enzyme.  
FT DOMAIN 1 250  
FT DOMAIN 271 548  
FT NP\_BIND 12 37  
FT ACT\_SITE 154 154  
FT NP\_BIND 280 304  
FT ACT\_SITE 420 420  
FT SEQUENCE 548 AA; 57593 MW; 399598C5DF17C23F CRC64;

Query Match 22.5%; Score 294.5; DB 1; Length 548;  
Best Local Similarity 33.6%; Pred. No. 1.2e-15;  
Matches 86; Conservative 41; Mismatches 100; Indels 29; Gaps 8;

QY 10 GVAIVTGGASGLATATRLVGGASAVLIDLPNSGGEAQAARKLNCCVAPADVTSEK 69  
Db 9 GRVIVTGAAGIGALVDIFANDDVYAVDLPPSGVIELGQNGEFGHLEGVDSHED 68  
QY 70 DVQATLAKKGFGRVAVANCAGT---AVASKTYNKKGGTHTLEFQRLVDVNLGT 125  
Db 69 DVVALEALKERFSRIEVLVNNAGIGPTMAATADT-----ALDEFQALALNIVGA 119

QY 126 FNVIRLVAGEMQNEPDGQGVYIINTASVAAREGGVGAAYASAKSGIVGMPLIARD 185  
Db 120 YSVACETAKLM---KFG-----AIVNVAASLAGLGNKRSAAYASAKSLSTRKLACR 171  
QY 186 LAPIGIRVKTIPGFGFPPLTSLPEKY-----CNFLAQVFPFPLSPAPAYAHLYO--A 239  
Db 172 WASRGIRVAVAPGAVHRTPEVAEL-ERAGKIDVSAIRRVPL-GRIRAPDEIRARVPELA 229  
QY 240 ILENPFLNGEVRIDG 255  
Db 230 SNAQASTIGSTILVDG 245

RESULT 18  
BA7L\_EUBSP  
ID BA7L\_EUBSP STANDARD; PRT; 249 AA.

AC P07914;  
DT 01-APR-1988 (Rel. 08, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) (Bile acid  
DE 7-dehydroxylase) (7-alpha-HSDH) (Bile acid-inducible protein).  
GN BA1A1 AND BA1A3.  
OS Eubacterium sp. (strain VPI 12708).  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
CC Clostridium.  
OX NCBI\_taxid=29347;  
RN [1]  
RP SEQUENCE FROM N.A. (BA1A3).  
RX MEDLINE=9030548; PubMed=2376563;  
RA Gopal-Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.;  
RT "Multiple copies of a bile acid-inducible gene in Eubacterium sp.  
RT strain VPI 12708";  
RL J. Bacteriol. 172:4420-4426(1990).  
RN [2]  
RP SEQUENCE FROM N.A. (BA1A1).  
RX MEDLINE=88197993; PubMed=2834320;  
RA Coleman J.P., White W.B., Lajewski M., Hylemon P.B.;  
RT "Nucleotide sequence and regulation of a gene involved in bile acid  
RT 7-dehydroxylation by Eubacterium sp. strain VPI 12708";  
RL J. Bacteriol. 170:2070-2077(1988).  
RN [3]  
RP SEQUENCE OF 1-55 FROM N.A. (BA1A1), AND SEQUENCE OF 1-33.  
RX MEDLINE=87165759; PubMed=354693;  
RA Coleman J.P., White W.B., Hylemon P.B.;  
RT "Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp.  
RT strain VPI 12708";  
RL J. Bacteriol. 169:1516-1521(1987).  
CC -1- FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID. YIELDING  
CC DEOXYCHOLIC ACID AND LITHOCHOLIC ACID. RESPECTIVELY. HIGHEST  
CC AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID.  
CC -1- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-  
CC cholanoate + NAD(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-  
CC cholanoate + NADH.  
CC -1- PATHWAY: Bile acid catabolism.  
CC -1- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A  
CC 7-ALPHA-HYDROXY GROUP.  
CC -1- SIMILARITY: THERE ARE THREE GENES FOR BAIL PROTEINS: BA1A1 IS  
CC IDENTICAL TO BA1A3 AND THERE IS 81% IDENTITY WITH BA1A2.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY.  
CC  
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CC  
CC EMBL: M34658; AAB61155.1; -.  
DR EMBL: M19654; AAB61154.1; -.  
DR EMBL: M15813; AAB61153.1; -.

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MEDLINE-98044033; PubMed-938437;
RA Kunst F., Ogassawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Beterio M.G., Bessieres P., Bolotin A., Borchet S.,
RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capiano V., Carter N.M.,
RA Choi S.K., Codani J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denioz F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Enlian K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
RA Filtz C., Fujita M., Fujita T., Funa S., Gallizi A., Galeon N.,
RA Gilm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grand G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Kleier-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kunita K., Lapius A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Melido R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Portoullik S., Prescott A.M.,
RA Priesean E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivoita C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone B.,
RA Sekiguchi J., Sekowska A., Serró S.J., Serró P., Shin B.S., Soldo B.,
RA Sorokin A., Taconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpsita P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambit R., Wedler E., Wedler H., Weitenegger T.,
RA Witters P., Wipat A., Yamamoto H., Yamane K., Yasunoko K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zanchin A.,
RA "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
DR EMBL: X73124; GAA51638.1; -
DR EMBL: 299123; CAB15799.1; -
DR PIR: S39737; S39737.
DR HSP: P50162; IAE1.
DR Subtilisin; BG10628; ywED.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRPFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
DR Hypothetical protein; Oxidoreductase; Complete proteome.
FW NP_BIND 11 33 NAD OR NADP (By SIMILARITY).
FT ACCT_SITE 154 154
SQ SEQUENCE 255 AA; 27324 MW; 20AA2259BFB8C9B CRC64;
Query Match 23.0%; Score 301; DB 1; Length 255;
Best Local Similarity 32.7%; Pred. No.1.6e-16;
Matches 88; Conservative 42; Mismatches 99; Indels 46; Gaps 8;
QY 14 VITGASGLGATTAERLVGQASAVLLDLPNSGGEAQAQKIGNNCV-FAPADVTSEKYO 72
DB 11 IITGASGSGYAAVAFIAGQCANVVADIDEAGSAMRKENDRLHFGVDITIDEAQC 70
QY 73 TALALAKGFGVADVAVNCAGIAVASKTYNLKGGTHLEDPORVLVDYINLGTENVIR- 130
DB 71 HAVESAVHTFTGLDLVNLNAGIEIYAPHEMF-----LSDMNKVLQVNLIGMFLMSHA 124
QY 131 ---LVAGEMGQNEPDQGGQGVITINTASVAAFEGVQGAAYASASKGIVGTEPIARDL 186
DB 125 LKHEMLAAG-----KGNITNTCSVSGVLVAMPDIPAYNASKGVLTQLTKSMADV 172

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QY 187 APIGIRVMTIAPGLFPTPLTSLPEKVCNFTL-----ASQVFPFSRLGDPAEY 233
DB 173 AKHQIRVNCVCGIITDP-----LNK-----SFLENNGTLEIKKAKVNPILRLGKPEEI 226
QY 234 AHVQALIE--NPINGEYIRIDGAIKQ 260
DB 227 ANVMFLASDLSSYMTGSAITADGGYTAQ 255
RESULT 16
ID 2BHD_STREX STANDARD; PRT; 255 AA.
AC 2BHD_STREX
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
OS Streptomyces exfoliatus (Streptomyces hydrogenans).
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1905;
RN [1]
RP SEQUENCE.
RX MEDLINE-90306362; PubMed-2194840;
RX Marekov L., Krook M., Joernvall H.;
RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
RT 'short-chain, non-metalloenzyme' alcohol dehydrogenase type."
RL FEBS Lett. 266:51-54(1990).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RP MEDLINE-92052211; PubMed-1946424;
RA Chosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
RA Rimsay R.L., Orr J.C.;
RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
RT dehydrogenase: a member of a short-chain dehydrogenase family."
RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
CC -1- CATALYTIC ACTIVITY: Androstane-3-alpha,17-beta-diol + NAD(+) = 17-
CC beta-hydroxyandrostane-3-one + NADH.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR PIR: S10707; S10707.
DR PDB: 2HSD; 31-AUG-94.
DR PDB: 1HDC; 07-FEB-95.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRPFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
DR Oxidoreductase; NAD; Steroid metabolism; 3D-structure.
FW NP_BIND 10 34 NAD (By SIMILARITY).
FT ACCT_SITE 152 152
SQ SEQUENCE 255 AA; 26484 MW; 90B93CB66AA628D5 CRC64;
Query Match 22.8%; Score 299; DB 1; Length 255;
Best Local Similarity 33.6%; Pred. No.2.3e-16;
Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;
QY 8 VKGLVAITVITGASGLGATTAERLVGQASAVLLDLPNSGGEAQAQKIGNNCVFAPADVT 67
DB 4 LSGKTVITITGASGLGATTAERLVGQASAVLLDLPNSGGEAQAQKIGNNCVFAPADVT 63
QY 68 EKDVTALALAKGFGVADVAVNCAGIAVASKTYNLKGGTHLEDPORVLVDYINLGTENVIR- 127
DB 64 EEDQVAVAAAREFGSGVDLVNAGISTMFL-----FTSEYERFRKVVADLVGVFI 117
QY 128 VIRLVAGEMGQNEPDQGGQGVITINTASVAAFEGVQGAAYASASKGIVGTEPIARDL 187
DB 118 GMKTVIVAM-----KDAAG--GSIVNISSAAGLGLATISYSGASKWGVRLSKLAAYELG 171
QY 188 PIGIRVMTIAPGLFPTPLT--TSLPEVCNFTLASQVFPFSRLG--DPAEYAHVQALIE-- 242
DB 172 TDIRVNSVHVGMTYTPMTAETGIRQEGNY--PNTPM--GRVAGNEPELIGAAVYKILSDT 228

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NP BIND 9 33 NADP (BY SIMILARITY).  
 ACT SITE 154 154 BY SIMILARITY.  
 FT ACT SITE 23 23 D -> A (IN REF. 1).  
 SQ SEQUENCE 246 AA; 26282 MM; C6A391167D237DC CRC64;  
 Query Match 23.6%; Score 309.5; DB 1; Length 246;  
 Best Local Similarity 29.7%; Pred. No. 3.3e-17;  
 Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;

13 AVITGGASGIGLTAELVVGOGASAVILDPNSGSGAQA-----KRIQNNCVFAPAV 65  
 7 AIVTGASRGIGRSTALDLAKSGANV---VNSGNEKANEVDEIKSMGRKAIKADY 63  
 66 TSEKDYOTATLALAKGKRGVAVNAGIAVASKTYNLKGGOTHTLEDFORVLDVNLMT 125  
 64 SNPEDVQNMKEITLVSFTIDILVNNAGITRDMLIMKE-----DEMDDVINIMKGV 117  
 126 PNVIATLVAGEMGONEPDGOGORVITNTASVAFEGVQGAASAKSGIVGWTLPARD 185  
 118 FNCTKAVTRQMKO-----RSGRIINWSSIVGSGNPGQANTYAAAGVIGLTKSSAKE 171  
 186 LAPIGIVMTIAPLFTGPTPLTSLPERKVCNFIASQVFPFRLDPAEYAHVQAITE-- 243  
 172 LASNIIVYNAIAPFISTDMTKLAKVDQEMLKQIPL-ARFGEPSDVSSTVFLASEGA 230  
 244 PFLNGEVIIRLDGAIM 259  
 231 RYMTGQTLDIDGMMV 246

RESULT 14  
 YK02\_MYCTU STANDARD; PRT: 260 AA.  
 AC 010855; 1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 38, Last sequence update)  
 DT 15-JUN-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative oxidoreductase Rv2002 (EC 1.-.-.-).  
 GN FMBG3 OR RV2002 OR MT2058 OR MTCX39.16C.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinobacteriales; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RC MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Kaula F., Badcock K., Besham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Kirogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."  
 RT Nature 393:537-544 (1998).  
 RL [2]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN-CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Dvortack T., Weidman J., Kouri H., Gill J., Mikula A., Bishai W.;  
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."  
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
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 DR EMBL; 274025; CAA98414.1; -  
 DR EMBL; AE007057; AAK46335.1; -  
 DR HSSP; E19992; LHDC.  
 DR TIGR; MT2058; -  
 DR Tuberculist; Rv2002; -  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.  
 FT NP BIND 11 35 NAD (BY SIMILARITY).  
 FT ACT SITE 153 153 BY SIMILARITY.  
 FT CONFLICT 174 174 S -> G (IN REF. 2).  
 SQ SEQUENCE 260 AA; 27030 MM; 0935A14ED36220B7 CRC64;  
 Query Match 23.3%; Score 305; DB 1; Length 260;  
 Best Local Similarity 33.9%; Pred. No. 7.9e-17;  
 Matches 85; Conservative 41; Mismatches 99; Indels 26; Gaps 5;

10 GLVAVITGGASGIGLTAELVVGOGASAVILDPNSGSGAQAARKLGNVCVAPADVTEK 69  
 7 GKVALYSGARGMGASHVAMAEKAYFGSIIDEBGKAAVALADARVTHLDVTPA 66  
 70 DVOTATLALAKGKRGVAVNAGIAVASKTYNLKGGOTHTLEDFORVLDVNLMTFNV 129  
 67 QMTAAVDTAFTAFGLHVLVNNAGI-----LNTGIEDYALTEQRIIDVNLTVFEG 120  
 130 RLIVAGEMGONEPDGOGORVITNTASVAFEGVQGAASAKSGIVGWTLPARDLAPI 189  
 121 RAVV-----KPKKENGKRSIIINISIEGLAGTVACHGTAKRFAVRGLTKSTALELGS 174  
 190 GIRVMTIAPGLFTGPTPLTSLPERKVCNFIASQVFPFRLDPAEYAHV--QATINP 244  
 175 GIIVNSIHPLGLVTPMTDWPEDI-----FQTALGRAAPEVSNLVYVYLADESS 225  
 245 FLNGEVIIRLDG 255  
 226 YSTGAEPVVDG 236

RESULT 15  
 YWFD\_BACSU STANDARD; PRT: 255 AA.  
 AC P39640;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical oxidoreductase ywfd (EC 1.-.-.-).  
 GN YWFD OR IPA-82D.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN-168;  
 RC MEDLINE=95020537; PubMed=7934828;  
 RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W., Hullo M.F., Ionescu M., Lubochinsky B., Marcelinsky L., Moszer I., Prescecian E., Santana M., Schneider E., Schweizer J., Vertes A., Rapoport G., Dancu A.;  
 RA "Bacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees."  
 RT Mol. Microbiol. 10:371-384 (1993).  
 RL [2]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN-168;

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DR EMBL: U34072; AAC53573.1; -  
 DR EMBL: U34072; AAC53574.1; -  
 DR EMBL: AF100956; AAC69902.1; -  
 DR HSSP: C70351; 1E6W  
 DR MGD; MG195911; H2-K66.  
 DR InterPro: IPR002196; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 KM Steroid biosynthesis; Oxidoreductase; NAD; Multigene family;  
 Alternative splicing.  
 FT NP\_BIND 13 38 NAD (BY SIMILARITY).  
 FT ACT\_SITE 168 168 GLPM -> MPRSMGGGOENTQYVMEK (IN LONG  
 FT VASAPLIC 257 260 ISOFORM).  
 FT CONFLICT 16 16 G -> GSGVPSQ (IN REF. 3).  
 FT CONFLICT 17 17 MISSING (IN REF. 1).  
 FT CONFLICT 230 230 E -> EG (IN REF. 1).  
 SQ SEQUENCE 260 AA; 26645 MW; 19C712FCDD168B08 CRC64;  
 Query Match 23.9% Score 313.5; DB 1; Length 260;  
 Best Local Similarity 31.0%; Pred. No. 1.7e-17;  
 Matches 85; Conservative 54; Mismatches 106; Indels 29; Gaps 9;  
 QY 1 MAACRSKGLVAVITGGA-SGLGLATAERLVGCGASAVLLDPNSGGEAQAQKLN--- 56  
 DB 1 MASQLR-LRSALALVTGAGSGICRAISVRLAEGAANAODLDGAACQTVRLTSGPS 59  
 QY 57 -----NCVFADADVTSEKDVCTALALAKGKFG-VDYAVNACGAGVASKIYNLKKQ 107  
 DB 60 EDGAPRGKHAAF-QADVSQGPARRRLLEVOACPSRPSPVYVSCAGITRDEFLHME-- 116  
 QY 108 THLTEDPQRYVDVNLMTGFENYRLVAGBMQNEPDGQSGVINTASVAFEGVGOAA 167  
 DB 117 -----EDMDRVAVNLKGFILVTOAAQAIVSS-----GGRSIIINISIIIGKXVNIQTN 167  
 QY 168 YSASKGIVGWTLPIDAPLIGIRVMTIAPGLFETPLILSLPKVCNPLASQVPPFSRL 227  
 DB 168 YASSAGVIGLITQFAARLGRGIRCNCSVLPFTIATPTQKMPKVDKVTAMPL-GRM 226  
 QY 228 GDPAEVAHVQ--AIIENPFLNGEYIRLDGIRFM 259  
 DB 227 GDPEDVADVAVFLASSEDGTYTGAASVEVSGGLFM 260

## RESULT 13

FABG\_BACSU

ID FABG\_BACSU STANDARD: PRT: 246 AA.

AC P51831.0311733; (rel. 34, Created)  
 DT 01-OCT-1996 (rel. 37, Last sequence update)  
 DT 15-DEC-1998 (rel. 41, Last annotation update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-  
 acyl carrier protein reductase).  
 GN FABG.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI-TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=168;  
 RX MEDLINE=96326321; PubMed=8759840;  
 RT Moridoni H.R., de Mendoza D., Cronan J.E. Jr.;  
 RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of  
 RT lipid biosynthesis genes";  
 RT J. Bacteriol. 178:4794-4800(1996).

## SEQUENCE FROM N.A.

RC STRAIN=168;  
 RC MEDLINE=96044033; PubMed=9384377;  
 RX Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RX Azevedo V., Bertero M.G., Bessieres P., Bojolt A., Borchert S.,  
 RX Boriss R., Bourlier L., Brans A., Braun M., Brigelli S.C., Bron S.,  
 RX Broutlet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,  
 RX Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
 RX Denzot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T.,  
 RX Enlian K.D., Erington J., Fabre C., Ferrari E., Foulger D.,  
 RX Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RX Gilm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,  
 RX Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RX Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RX Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RX Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RX Kurita K., Lapidus A., Lardinois S., Lauder J., Lazarevic V.,  
 RX Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RX Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RX Noone D., O'Reilly M., Ogawa K., Ogilawa A., Oudega B., Park S.H.,  
 RX Parro V., Pohl T.M., Portetle D., Porwollik S., Prescott A.M.,  
 RX Presecan E., Puig P., Purrelle B., Rapoport G., Rey M., Sadale Y.,  
 RX Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,  
 RX Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RX Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Solito B.,  
 RX Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RX Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P., Tognoni A.,  
 RX Toso V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
 RX Viart A., Wambit R., Wedler E., Medler H., Wetzenecker T.,  
 RX Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RX Yoshida K., Yoshikawa H.F., Zimstein E., Yoshikawa H., Danchin A.,  
 RT "The complete genome sequence of the Gram-positive bacterium  
 RT Subtilis";  
 RT Nature 390:249-256(1997).  
 RL [3]  
 RP SEQUENCE OF 1-172 FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98195738; PubMed=9534246;  
 RA Foulger D., Erington J.;  
 RT "A 28 kbp segment from the spvM region of the Bacillus subtilis 168  
 RT genome";  
 RL Microbiology 144:801-805(1998).  
 RN [4]  
 RP SEQUENCE OF 230-246 FROM N.A.  
 RC STRAIN=168;  
 RA Oguro A., Kakeshita H., Takamatsu H., Nakamura K., Yamane K.;  
 RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RL CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -I- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC PATHWAY.  
 CC -I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
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AC Q92506; Q9UIQ1;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-  
 beta-hydroxysteroid dehydrogenase 8) (K66 protein) (K6-6).  
 GN HSD17B8 OR HKE6 OR RING2 OR FABGL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tubby B.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 3-261 FROM N.A.  
 RX MEDLINE=97001166; PubMed=8812499;  
 RA Ando A., Kikuchi Y.Y., Shigenari A., Kawata H., Okamoto N., Shina T.,  
 Chen L., Ikemura T., Abe K., Kimura M., Inoko H.,  
 "cDNA cloning of the human homologues of the mouse K64 and K66 genes  
 at the centromeric end of the human MHC region."  
 RL Genomics 35:600-602(1996).  
 CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.  
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +  
 NAD(P)H.  
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.  
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE LIVER AND PANCREAS,  
 LOWER IN THE SKELETAL MUSCLE AND KIDNEY.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 (SDR) FAMILY.  
 CC CC  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC CC  
 DR EMBL: AL031228; CAC38444.1;  
 DR EMBL: DB2061; BAAL1529.1;  
 DR HSBP; O70351; IEGW.  
 DR GeneW; HGNC:3554; HSD17B8.  
 DR MIM: 601417;  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT.1.  
 KM Steroid biosynthesis; Oxidoreductase; NAD; Multigene family.  
 FT NP\_BIND 15  
 FT ACT\_SITE 169  
 FT CONFLICT 117  
 FT CONFLICT 193  
 FT CONFLICT 208  
 FT CONFLICT 212  
 FT SEQUENCE 261 AA; 888B2D7131714D71 CRC64;  
 SQ  
 Query Match 25.4%; Score 332.5; DB 1; Length 261;  
 Best Local Similarity 31.2%; Pred. No. 5.9e-19;  
 Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;  
 DB 8 VKGIVAVITGGASGIGLATFAERLVGGSASVLLDIPNSGGEAQAARKL-----GN 56  
 DB 9 LRSALAVITGAGSGIGRAVSRLAGEATVACIDLRRAAETVRLVLLGPGSKSGPPPGN 68  
 DB 57 NCVEPADVTSKEDVQALALAKRFGK-VDVAVNCAGIAVASKTYLNKKQGTHTLEDFQ 115  
 DB 69 HAAF-QADVSEARARCLLEGVQACFSRPPSVVASCAGITODEFLHMS-----DDWD 121  
 DB 116 RVLVDVNGTFTVIVLVAGEMGQNPDPGGGQGVVIVNNSVAAPFGGVGAAYASAKGCI 175  
 DB 122 KVIAVNLKGTFLVTAALAAVSN-----GCGSTIINISIVGKGVNGQVYASKAGV 176

QY 176 VENTLPIARDLAPIGIRVNTIAPGLGPELLTSLPEKYCNLTASQVPPPSRLGPAEYAH 235  
 DB 177 IGLTQFAARELRHGRHCRNSVLPGLFIAFMTOKVPQKVDKITEMIPM-GRIGDEPDVAD 235  
 QY 236 LVO--ALLENPLNGEVIRLDGAIIR 259  
 DB 236 VVAFLASDSGYITGTSVEITGLFP 261  
 RESULT 10  
 ID FABG\_VIBCH STANDARD; PRI: 244 AA.  
 AC Q9KQJ7;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-  
 acyl carrier protein reductase).  
 GN FABG OR VC2021  
 OS Vibrrio cholerae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.  
 NX NCBI\_TaxID=666;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=El Tor N16961 / Serotype O1;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Ungey L.A.,  
 Gill S.R., Nelson K.E., Read T.D., Fetsch H., Richardson D.,  
 Emdolaeva M.D., Yatchew J., Bass S., Qin H., Drago I., Sellers P.,  
 McDonald L., Utterback T., Fleischmann R.D., Nielsen W.C., White O.,  
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 Fraser C.M.;  
 RA "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*  
 cholerae".  
 RL Nature 406:477-483(2000).  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 PATHWAY.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 (SDR) FAMILY.  
 CC CC  
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 CC CC  
 DR EMBL: AE004276; AAF95169.1; ALT\_INT.  
 DR HSBP; P19992; IHDC.  
 DR TIGR; VC2021;  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT.1.  
 KM Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.  
 FT NP\_BIND 10  
 FT ACT\_SITE 34  
 FT SEQUENCE 151 AA; 9FB2B278D7CC3CE CRC64;  
 SQ  
 Query Match 25.1%; Score 328.5; DB 1; Length 244;  
 Best Local Similarity 32.0%; Pred. No. 1.1e-18;  
 Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;  
 DB 7 SVKGIIVAVITGGASGIGLATFAERLVGGSASVLLDIPNSGGEAQAARKGNNVFAPADVT 66  
 DB 2 NLEKVALVIGASGIGKAIELAEKAGAVIGTATSESGAQAISDYLDGNGGMLNVT 61  
 QY 67 SKDVQALALAKRGRVDVAVNCAGIAVASKTYLNKKQGTHTLEDFQVRLVDMGT 126

RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,  
 RA Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 genome sequence of *Thermococcus maritima*.";  
 RL Nature 398:323-329(1999).  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC PATHWAY.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
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 CC -----  
 CC EMBL: AE001811; AAD36790.1; -  
 CC DR HSSP: P50162; IAEI.  
 CC DR TIGR: TM1724; -  
 CC DR InterPro: IPR002198; ADH\_short.  
 CC DR Pfam: PF00106; adh\_short; 1.  
 CC DR PRINTS: PR00080; SDRFAMILY.  
 CC DR PROSITE: PS00061; ADH\_SHORT; 1.  
 CC DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.  
 CC KW NP\_BIND 10 34 NADP (BY SIMILARITY).  
 CC FT ACT\_SITE 154 154 BY SIMILARITY.  
 CC FT SEQUENCE 246 AA; 26401 MW; 8008904D28099142 CRC64;  
 CC SQ  
 CC Query Match 26.1%; Score 341; DB 1; Length 246;  
 CC Best Local Similarity 33.7%; Pred. No. 1,2e-19;  
 CC Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;  
 CC  
 CC QY 8 VKGLAVITGASGLGATLAEVLVQGSASAVLDLPNSGGA---QAKKLGNNVFRPAD 64  
 CC DB 3 LEGKVLITGASAGIGKATTLTLLFAQEGATVAGISKNLSTLVKEAEGPGRKADPYVLN 62  
 CC QY 65 VTSEKDVOTLALAKGKRGVAVNCAVAGIAVASKTYLKKQGTHTLEDFORVLDVNLNG 124  
 CC DB 63 VTDROIKVEYKVKQKGRIDVLYNNNGITRDALVAMKE-----EDMVAIVNLNG 116  
 CC QY 125 TENVRLVAGENGQNEPDGQGVYINTASVAAEFGGVQAAYSASKSGIVGKTLPIAR 184  
 CC DB 117 VENVYQMVVPMYIKQ-----KNGSIVAVSSVVGIGNPQNTNYSASRAGVIGMTKRWAK 170  
 CC QY 165 DIAPGIVMTAPLFGFTPLTSLPEKVCNPLASQVFPSPRLGDPAPAYAHV--QAIIIE 242  
 CC DB 171 ELAGNNIRNNAVAPGFTIETPEKRLPEKARETALSRIPL-GRFGPEVAYQVILFLASDE 229  
 CC QY 243 NPELNGEYIRLDGAI 257  
 CC DB 230 SSYVTGVYIGIDGGL 244  
 CC  
 CC RESULT 8  
 CC FABG\_CUPLA STANDARD; PRT; 320 AA.  
 CC ID P28643;  
 CC AC 01-DEC-1992 (Rel. 24, Created)  
 CC DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE 3-oxoacyl-[acyl-carrier protein] reductase, Chloroplast precursor  
 CC (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).  
 CC GN CLKR27.  
 CC OS Cuphea lanceolata.  
 CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eucosids II; Myrtales; Lythraceae; Cuphea.  
 CC NCBI\_TaxID=3930;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=92293104; PubMed=1376402;  
 CC RA Klein B., Pawlowski K., Hoerlcke-Grandpierre C., Schell J.,  
 RA Toepfer R.;  
 RT "Isolation and characterization of a cDNA from *Cuphea lanceolata*  
 RT encoding a beta-ketoacyl-ACP reductase.";  
 CC M01. Gen. Gene. 233:122-128(1992).  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC PATHWAY.  
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC  
 CC PLASTIDS.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
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 CC -----  
 CC EMBL: X64566; CAA45866.1; -  
 CC DR PIR: S19832; S19832.  
 CC DR HSSP: P50162; IAEI.  
 CC DR InterPro: IPR002198; ADH\_short.  
 CC DR Pfam: PF00106; adh\_short; 1.  
 CC DR PRINTS: PR00080; SDRFAMILY.  
 CC DR PROSITE: PS00061; ADH\_SHORT; 1.  
 CC DR Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast;  
 CC KW Transist peptide.  
 CC FT TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).  
 CC FT CHAIN 62 320 3-OXOACYL-[ACYL-CARRIER PROTEIN]  
 CC FT NP\_BIND 82 106 NADP (BY SIMILARITY).  
 CC FT ACT\_SITE 227 227 BY SIMILARITY.  
 CC FT SEQUENCE 320 AA; 33103 MW; 06BAF052B2B8C87 CRC64;  
 CC SQ  
 CC Query Match 25.5%; Score 334; DB 1; Length 320;  
 CC Best Local Similarity 32.7%; Pred. No. 5.7e-19;  
 CC Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;  
 CC  
 CC QY 2 AAACRSYKGLAVITGASGLGATLAEVLVQGSASAVLDLPNSGGA---QAKKLGN 56  
 CC DB 69 AGAGOSVSEPVVITGSRIGKALSL-GKAGCVLVNARSSEAEVSKIEAFQ 127  
 CC QY 57 NCYFAPADVSEKDVOTLALAKGKRGVAVNCAVAGIAVASKTYLKKQGTHTLEDFOR 116  
 CC DB 128 QALTFGGDVSKEDVEMITAYDANGTYDILVNNAGITDGLMKRKSQ-----WQE 181  
 CC QY 117 VLDVNLNGTFENVRLVAGENGQNEPDGQGVYINTASVAAEFGGVQAAYSASKSGIV 176  
 CC DB 182 VIDNLNGVFLCTQAAKIMKK-----KKGRIINIASVVGIVGNAGQANTYSAAAGYI 235  
 CC QY 177 GMTLPFARDLAPGIRVMTAPLFGFTPLTSLPEKVCNPLASQVFPSPRLGDPAPAYAHV 236  
 CC DB 236 GFTYVAREYASRNINNAVAPGFISDMSKIDDKINKILLETPL-GRYGPPEVAYGL 294  
 CC QY 237 VQAIENP---FLNGEYIRLDGAI 259  
 CC DB 295 VEFIAINPSSVYGVFTIDGGM 320  
 CC  
 CC RESULT 9  
 CC DH88\_HUMAN STANDARD; PRT; 261 AA.  
 CC ID DH88\_HUMAN



OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA;  
 RA Fu J., Chen X., Stern D., Yan S. D.;  
 RL Submitted (Apr.1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 DR EMBL: U96116; AAB57689.1; ALT\_INIT.  
 DR HSP: 070351; 1B6W.  
 DR SWISS-2DPAGE: 008756; MOUSE.  
 DR MGD: MGI:1333871; Hsd17b10.  
 DR InterPro: IPR002198; Adh\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Oxidoreductase; NAD.  
 KW NP\_BIND  
 FT ACT\_SITE 168  
 FT SEQUENCE 261 AA; 27418 MW; 61231B1E2839D41 CRC64;  
 SQ  
 Query Match 86.5%; Score 1133; DB 1; Length 261;  
 Best Local Similarity 86.2%; Pred. 1.53e-81;  
 Matches 225; Conservative 19; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 MAAACRSYKGLVAVITGASGLGIAERLVGGASAVLLDPSNGGEAQAQKLNCF 60  
 DB 1 MAAVRSYKGLVAVITGASGSPWATKRLVGGATVLLDPSSEGEQAQKLGSCIF 60  
 QY 61 ARAVTEKDYQVTLALAKGFGVDVAVNACAGAVASKTNNKGGOTHTLEFORL 120  
 DB 61 ARAVTEKDYQVTLALAKGFGVDVAVNACAGAVASKTNNKGGOTHTLEFORL 120  
 QY 121 NLMGTENVIRLVAGEMQNEPDGQGRGVIIINTASVAEPFGVGOAAVSASKGI 180  
 DB 121 NLMGTENVIRLVAGEMQNEPDGQGRGVIIINTASVAEPFGVGOAAVSASKGI 180  
 QY 121 NLMGTENVIRLVAGEMQNEPDGQGRGVIIINTASVAEPFGVGOAAVSASKGI 180  
 DB 121 NLMGTENVIRLVAGEMQNEPDGQGRGVIIINTASVAEPFGVGOAAVSASKGI 180  
 QY 181 PIADIDPIGIRVWTIAPGLGFTPLTSLPEKVCNFTASOVPEPSRLGDPAEVA 240  
 DB 181 PIADIDPIGIRVWTIAPGLGFTPLTSLPEKVCNFTASOVPEPSRLGDPAEVA 240  
 QY 241 IENPFLNGEVIRLDGAIRMOP 261  
 DB 241 IENPFLNGEVIRLDGAIRMOP 261  
 ID HCD2\_DROME STANDARD; PRT; 255 AA.  
 AC 018404;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
 DE (Scully protein).  
 GN SCU OR CG7113.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LEU-33 AND PHE-120.  
 RC STRAIN=Canton-S;  
 RX MEDLINE=98252852; PubMed=9585418;  
 RA Torroja L., Ortuno-Sahagun D., Ferrus A., Haemmerle B., Barbas J.A.;  
 RT Scully, an essential gene of Drosophila, is homologous to mammalian  
 RT mitochondrial type II L-3-hydroxyacyl-CoA dehydrogenase/amyloid-beta  
 RT peptide-binding protein.  
 RL J. Cell Biol. 141:1009-1018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.Y.,  
 RA Brandon R.C., Rogers J.H.C., Blazey R.G., Chape M., Pfeiffer B.D.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borovna D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,  
 RA Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Flosser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Idegawa C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paabo S.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT The genome sequence of Drosophila melanogaster.  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: MAY PLAY A ROLE IN GERM LINE FORMATION.  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC -1- SUBUNIT: MULTIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).  
 CC -1- TISSUE SPECIFICITY: FOUND IN MANY TISSUES INCLUDING CNS. HIGHEST  
 CC EXPRESSION IN BOTH EMBRYONIC GONADAL PRIMORDIA AND MATURE OVARIES  
 CC AND TESTES.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
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 CC -----  
 DR EMBL: Y15102; CAA75377.1; -

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CC EMBL: AB002156; BAA19510.1; -  
 CC HSSP: 070351; 1E6W;  
 CC InterPro: IPR002198; ADH\_short.  
 CC Pfam: PF00106; adh\_short; 1.  
 CC PRINTS: PR00080; SDRFAMILY.  
 CC PROSITE: PS00061; ADH\_SHORT; 1.  
 CC Oxidoreductase; NAD; Mitochondrion.  
 CC NAD BIND  
 CC ACT\_SITE 168 168 NAD (BY SIMILARITY).  
 CC SEQUENCE 261 AA; 27140 MW; 807572B6A9A49780 CRC64;

Query Match 92.1%; Score 1206; DB 1; Length 261;  
 Best Local Similarity 92.0%; Pred. No. 9, 6e-87;  
 Matches 240; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGGASGLGATAEKLYGGAGASVLLDLPNSGGEAOKKLGNNCYF 60  
 DB 1 MAACRSYKGLVAVITGGASGLGATAEKLYGGAGATVLLDLPNSGGEAOKKLGNSCAP 60  
 QY APADVTSEKDVQVATLALAKGFGVDVAVNCAGIAVASKTYNKKQTHLEDFORVLDV 120  
 DB APADVTSEKDVQVATLALAKGFGVDVAVNCAGIAVASKTYNKKQTHLEDFORVLDV 120  
 QY 61 APADVTSEKDVQVATLALAKGFGVDVAVNCAGIAVASKTYNKKQTHLEDFORVLDV 120  
 DB 61 APADVTSEKDVQVATLALAKGFGVDVAVNCAGIAVASKTYNKKQTHLEDFORVLDV 120  
 QY 121 NLMTFENVIRLVAGEMQNEPDGQGGVITINTASVAFEGOVGOAAYSAKSGIYGMTL 180  
 DB 121 NLMTFENVIRLVAGEMQNEPDGQGGVITINTASVAFEGOVGOAAYSAKSGIYGMTL 180  
 QY 121 NLMTFENVIRLVAGEMQNEPDGQGGVITINTASVAFEGOVGOAAYSAKSGIYGMTL 180  
 DB 121 NLMTFENVIRLVAGEMQNEPDGQGGVITINTASVAFEGOVGOAAYSAKSGIYGMTL 180  
 QY 181 PIADLPIGIRVMTIAPGLTSLPEKVCNFIASQVPPSRRLGDPAEVAHLVQAI 240  
 DB 181 PIADLPIGIRVMTIAPGLTSLPEKVCNFIASQVPPSRRLGDPAEVAHLVQAI 240  
 QY 241 ENPFLNGEVTIRLDGAIKMP 261  
 DB 241 ENPFLNGEVTIRLDGAIKMP 261

RESULT 3  
 HCD2\_RAT STANDARD: PRT: 260 AA.  
 ID HCD2\_RAT STANDARD: PRT: 260 AA.  
 AC 070351; Q9QYD4;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
 DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).  
 GN HADH2 OR ERAB.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Gunn-Moore F.J., Tavaire J.M.;  
 RT "Rattus norvegicus amyloid beta-peptide binding protein (ERAB) mRNA";  
 RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RA Yang S.-Y., He X.-Y.;  
 RT "Molecular cloning and characterization of the cDNA of rat brain short chain L-3-hydroxyacyl-CoA dehydrogenase.";  
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RC TISSUE=Brain;  
 RA Powell A.J., Read J.A., Banfield M.J., Gunn-Moore F., Yan S.D., Lustrader J., Stern A.R., Stern D.M., Brady R.L.;

RA Lustrader J., Stern A.R., Stern D.M., Brady R.L.;

RT "Recognition of structurally diverse substrates by type II  
 RT 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding  
 RT alcohol dehydrogenase (ABAD).";  
 RL J. Mol. Biol. 303:311-327(2000).  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) -> 3-oxoacyl-CoA + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SCR) FAMILY.  
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CC EMBL: AF049878; AAC05747.1; -  
 CC EMBL: AF069770; AF14853.1; -  
 CC PDB: 1E3W; 25-MAY-01.  
 CC PDB: 1E3S; 25-MAY-01.  
 CC PDB: 1E6W; 25-MAY-01.  
 CC InterPro: IPR002198; ADH\_short.  
 CC Pfam: PF00106; adh\_short; 1.  
 CC PRINTS: PR00080; SDRFAMILY.  
 CC PROSITE: PS00061; ADH\_SHORT; 1.  
 CC Oxidoreductase; NAD; Acetylation; 3D-structure.  
 CC NAD BIND  
 CC ACT\_SITE 167 167 NAD (BY SIMILARITY).  
 CC CONFLICT 4 4 V -> C (IN REF. 2).  
 CC SEQUENCE 260 AA; 27114 MW; 30F7E723A95F9227 CRC64;

Query Match 87.9%; Score 1151; DB 1; Length 260;  
 Best Local Similarity 87.7%; Pred. No. 1, 8e-82;  
 Matches 228; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 2 MAACRSYKGLVAVITGGASGLGATAEKLYGGAGASVLLDLPNSGGEAOKKLGNNCYF 61  
 DB 1 MAACRSYKGLVAVITGGASGLGATAEKLYGGAGATVLLDLPNSGGEAOKKLGNSCAP 60  
 QY 62 PAVVTSEKDVQVATLALAKGFGVDVAVNCAGIAVASKTYNKKQTHLEDFORVLDV 121  
 DB 62 PAVVTSEKDVQVATLALAKGFGVDVAVNCAGIAVASKTYNKKQTHLEDFORVLDV 120  
 QY 122 LMGTENVIRLVAGEMQNEPDGQGGVITINTASVAFEGOVGOAAYSAKSGIYGMTL 181  
 DB 122 LMGTENVIRLVAGEMQNEPDGQGGVITINTASVAFEGOVGOAAYSAKSGIYGMTL 180  
 QY 182 IARDLPIGIRVMTIAPGLTSLPEKVCNFIASQVPPSRRLGDPAEVAHLVQAI 241  
 DB 182 IARDLPIGIRVMTIAPGLTSLPEKVCNFIASQVPPSRRLGDPAEVAHLVQAI 240  
 QY 242 ENPFLNGEVTIRLDGAIKMP 261  
 DB 242 ENPFLNGEVTIRLDGAIKMP 260

RESULT 4  
 HCD2\_MOUSE STANDARD: PRT: 261 AA.  
 ID HCD2\_MOUSE STANDARD: PRT: 261 AA.  
 AC 008756;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
 DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).  
 GN HADH2 OR HSD17B10 OR ERAB.  
 OS Mus musculus (Mouse).

HCD2\_HUMAN STANDARD; PRT; 261 AA.  
 AC 099714;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
 DE (Endoplasmic reticulum-associated amyloid beta-peptide binding  
 protein) (Short-chain type dehydrogenase/reductase XH9862).  
 GN HADH2 OR ERAB OR XH9862 OR SCHAD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE=97478528; PubMed=9338779;  
 RA Yan S.D., Fu J., Soto C., Chen X., Zhu H., Al-Mohanna F.,  
 RA Collinson K., Zhu A., Stern E., Saïdo T., Tohyama M., Ogawa S.,  
 RA Rohrer A., Stern D.;  
 RA "An intracellular protein that binds amyloid-beta peptide and  
 RT mediates neurotoxicity in Alzheimer's disease.";  
 RL Nature 389:689-695(1997).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RA Zhuchenko O.P., Wehnert M., Bailey J., Sun Z.S., Lee C.C.;  
 RA Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RN SEQUENCE FROM N.A.  
 RA MEDLINE=96837980; PubMed=9671743;  
 RA Miller A.P., Willard H.F.;  
 RA "Chromosomal basis of X chromosome inactivation: Identification of a  
 RT multigene domain in Xp11.21-p11.22 that escapes X inactivation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8709-8714(1998).  
 [4]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE=98221216; PubMed=9553139;  
 RA He X.Y., Schult H., Yang S.Y.;  
 RA "A human brain L-3-hydroxyacyl-coenzyme A dehydrogenase is identical  
 RT to an amyloid beta-peptide binding protein involved in Alzheimer's  
 RT disease.";  
 RL J. Biol. Chem. 273:10741-10746(1998).  
 [5]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: BINDS INTRACELLULAR AMYLOID-BETA. BY INTERACTING WITH  
 CC AMYLOID-BETA, IT MAY CONTRIBUTE TO THE NEURONAL DYSFUNCTION  
 CC ASSOCIATED WITH ALZHEIMER DISEASE.  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL TISSUES BUT IS  
 CC OVEREXPRESSED IN NEURONS AFFECTED IN AD.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SCR) FAMILY.  
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 CC -----  
 CC EMBL: U96132; AAC51812.1;  
 CC EMBL: U73514; AA868958.1;  
 CC EMBL: AF068134; AAC39900.1;  
 CC EMBL: AF035353; AAC15902.1;

DR EMBL: BC000372; AAH00372.1;  
 DR HSSP: O70351; IE3S.  
 DR Genew: HGNC:4800; HADH2.  
 DR MIM: 300256;  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: P50061; ADH\_SHORT; 1.  
 KW OXidoreductase; NAD.  
 FT NF\_BIND 12 37 NAD (BY SIMILARITY).  
 FT ACT\_SITE 168 168 BY SIMILARITY.  
 SQ SEQUENCE 261 AA; 26923 MW; 9E74F242E3E5EF1 CRC64;  
 Query Match 100.0%; Score 1309; DB 1; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-95;  
 Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAACRSYVGLVAVITGASGLATAEERLVGQASAVLLDLPNSGGEAARKLNQVF 60  
 DB 1 MAACRSYVGLVAVITGASGLATAEERLVGQASAVLLDLPNSGGEAARKLNQVF 60  
 QY 61 APADVTSEKDVCTALALAKGKGRVDVAVNCAIGVASTYTLKKGQHTLEDQFVLDV 120  
 DB 61 APADVTSEKDVCTALALAKGKGRVDVAVNCAIGVASTYTLKKGQHTLEDQFVLDV 120  
 QY 121 NLNGTFNVIRLVAGENGQNEPDGQGVYINTASVALEGGVGAAYSAKGIYGMTL 180  
 DB 121 NLNGTFNVIRLVAGENGQNEPDGQGVYINTASVALEGGVGAAYSAKGIYGMTL 180  
 QY 181 PIARDLAPIGIRMTAPGIFGTPLLTSLPEKVCNPLASQVPPSLGDPAEYAHVQAI 240  
 DB 181 PIARDLAPIGIRMTAPGIFGTPLLTSLPEKVCNPLASQVPPSLGDPAEYAHVQAI 240  
 QY 241 IENPFLNGEYIRLDGAIKMP 261  
 DB 241 IENPFLNGEYIRLDGAIKMP 261  
 RESULT 2  
 HCD2\_BOVIN STANDARD; PRT; 261 AA.  
 AC 002691;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).  
 GN HADH2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 [1]  
 RN SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RA MEDLINE=97214648; PubMed=9061026;  
 RA Futura S., Kobayashi A., Miyazawa S., Hashimoto T.;  
 RA "Cloning and expression of cDNA for a newly identified isozyme of  
 RT bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into  
 RT mitochondria.";  
 RL Biochem. Biophys. Acta 1350:317-324(1997).  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SCR) FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:47 ; Search time 7.83333 Seconds  
(without alignments)  
1381.956 Million cell updates/sec

Title: US-09-931-186-8  
Perfect score: 1309  
Sequence: 1 MAACRSVKGLVAVITGGAS.....ENPLNGEVIKLDGAIKMP 261

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1309	100.0	261	1	HCD2_HUMAN
2	1206	92.1	261	1	HCD2_BOVIN
3	1191	87.9	260	1	HCD2_RAT
4	1132	86.5	261	1	HCD2_MOUSE
5	908	69.4	255	1	HCD2_PROMY
6	383.5	29.3	247	1	YD50_MYCTU
7	341	26.1	246	1	FABG_THEMA
8	334	25.5	320	1	FABG_CUPHA
9	332.5	25.4	261	1	DH88_HUMAN
10	328.5	25.1	244	1	FABG_VIBCH
11	313.5	23.9	247	1	FAG1_SYNY3
12	313.5	23.9	260	1	DH88_MOUSE
13	309.5	23.6	246	1	FABG_BACSU
14	305	23.0	260	1	YK02_MYCTU
15	301	23.0	255	1	YKFD_BACSU
16	299	22.8	255	1	2BHD_STRPMY
17	294.5	22.3	249	1	Y4V1_RHISN
18	292	22.3	249	1	BAV1_EHBSF
19	291.5	22.3	244	1	FABG_VIBHA
20	290.5	22.2	248	1	FABG_AOUAE
21	289.5	22.1	244	1	FABG_ECOLI
22	288	22.0	263	1	UCPA_SALTY
23	287.5	22.0	246	1	PHBB_AICBU
24	286	21.8	246	1	PHAB_AICSP
25	284.5	21.7	256	1	Y019_THEMA
26	283.5	21.7	244	1	FABG_SALTY
27	281.5	21.5	246	1	NODG_AZOB
28	280	21.4	259	1	CMTB_PSEPU
29	279.5	21.4	241	1	PHBB_ZOORA
30	279.5	21.4	246	1	FABG_CHLMU
31	277.5	21.2	289	1	YHDE_BACSU
32	277	21.2	250	1	LINC_PSEPA
33					
34	276	21.1	263	1	UCPA_ECO57
35	276	21.1	263	1	UCPA_ECOLI
36	275	21.0	246	1	PHBB_CHRVI
37	272	20.8	250	1	LINC_PSEPA
38	272	20.8	319	1	FABG_ARATH
39	272	20.7	240	1	FABG_SYNY3
40	270.5	20.7	247	1	FABG_CHITR
41	270.5	20.7	247	1	FABG_CHITR
42	269.5	20.6	261	1	DH88_STRCM
43	268.5	20.5	262	1	DH88_BACME
44	267.5	20.4	336	1	TS2_MAIZE
45	266.5	20.4	241	1	PHBB_RHIME
46	266.5	20.4	242	1	FABG_HAEIN
47	264	20.2	247	1	FABG_MYCTU
48	261	19.9	261	1	DH88_BACME
49	259	19.8	258	1	DH82_BACSU
50	259	19.8	261	1	DH83_BACME
51	259	19.8	261	1	DH83_BACME
52	258	19.7	261	1	DH82_BACME
53	257.5	19.7	238	1	Y0XD_BACSU
54	257	19.6	256	1	BUDC_KLEPN
55	257	19.6	261	1	DH84_BACME
56	256	19.6	261	1	DH81_BACME
57	254.5	19.4	241	1	FABG_RICPR
58	254	19.4	261	1	SORD_KLEPN
59	251.5	19.2	267	1	PGDH_HUMAN
60	250.5	19.1	266	1	YHXC_BACSU
61	250.5	19.1	285	1	YAMP_RHISN
62	250	18.8	253	1	YAMP_RHISN
63	246.5	18.8	261	1	ACT3_STRCO
64	245.5	18.8	253	1	3BHD_COMTE
65	245	18.7	255	1	YV06_PSEAE
66	245	18.7	255	1	GNO_GLIOX
67	244.5	18.7	245	1	NODG_RHIS3
68	244.5	18.7	262	1	YXBG_BACSU
69	243	18.6	270	1	DHMA_FIAS1
70	241.5	18.4	258	1	BDHA_RHIME
71	239	18.3	255	1	BDHA_ECOLI
72	238	18.2	255	1	FABG_PSEAE
73	238	18.2	255	1	FABG_MYCAV
74	237.5	18.1	261	1	YGCW_ECOLI
75	237	18.0	248	1	FABG_CHLPN
76	235	18.0	257	1	YXJF_BACSU
77	228.5	17.5	245	1	NODG_RHIME
78	227.5	17.5	894	1	FOX2_NEUCR
79	227.5	17.4	258	1	BDHA_ALCBU
80	226.5	17.3	242	1	PHAB_PARDE
81	226.5	17.3	273	1	TRN1_DAIPT
82	224.5	17.2	249	1	DH82_STRVN
83	224.5	17.2	256	1	DH82_STRVN
84	224	17.1	254	1	IDNO_ECOLI
85	223.5	17.1	241	1	BUDC_KLEFE
86	222.5	17.0	256	1	MTDH_UROFA
87	222.5	17.0	87	1	FOX2_YEAST
88	222.5	17.0	900	1	FABG_MYCSM
89	221.5	16.9	285	1	GS39_BACSU
90	220.5	16.8	272	1	DH81_STRVN
91	219.5	16.8	248	1	SRLD_ECOLI
92	217	16.6	259	1	Y452_LISIN
93	217	16.6	254	1	KDUD_BACSU
94	216.5	16.5	253	1	KDUD_ECOLI
95	215	16.4	242	1	KDUD_ACTAC
96	213	16.3	134	1	DH88_CALT4
97	212.5	16.2	144	1	Y432_LISMO
98	212	16.2	281	1	BPBB_COMTE
99	212	16.2	281	1	YHND_BACSU
100	211.5	16.2	278	1	Y4LA_RHISN

## ALIGNMENTS



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DE 3-O-acetyl-(acyl-carrier protein) reductase (EC 1.1.1.100).  
GN FMBQ\_0182491. OS  
OS Bacillus halodurans.  
OC Bacteri; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86655;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132;  
RA Takem H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kihara S.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliophilic bacterium Bacillus  
RT halodurans and genomic comparison with Bacillus subtilis.";  
RT Nucleic Acids Res. 28:4317-4331(2000).  
CC 1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY.  
DR EMBL: AF001515; DAB06210.1; -  
DR HSSP: P19992; 1HDC.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short; 1.  
DR PRINTS: PRO0080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; UNKNOWN\_1.  
KW Oxidoreductase; Complete proteome.  
SQ SEQUENCE 246 AA, 26126 MW, 8525B5EB8BD9E90 CRC64;

Query Match	25.5%;	Score 333.5;	DB 16;	Length 246;
Best Local Similarity	34.2%;	Pred. No. 1.1e-15;		
Matches 90;	Conservative 42;	Mismatches 102;	Indels 29;	Gaps 7;

Qy	8	VKELVAVITIGGASGLIELIAERLVQGGASAVLTDLPNSGCE-----	AAQKLGANCVC	59
Db	2	LOGKTAIVTGASGICRATAMELARIKANVVV-----	NYAGNKEKAKEKVAIEIKFLGYEAL	57
Qy	60	FAPADATSERDVOGTALALAKGKEGRDVAVNCAGIAVASKYTNLKKGGTHLEDFQVLD		119
Db	58	AIGADVADESQVAMVKETIDTFEAGVADILVNNAGITRDNLEFRKKE-----	EDMDAVID	111
Qy	120	VNLMGFNVTIRYAGSGMGONEBDOGGR-GVYINASAAPEQGVQGAASASGCIYGM		178
Db	112	TNLKGFPHCKAKVTRPMK-----	QRGRIINISSVYGAIGNAGQANYAAAGVITGL	164
Qy	179	TLEIADLPAIGIRVNTIAPGLFEGPILSLTPEKCNCLASQVPEPSPGLDPAHYAHVQ		238
Db	165	TKLIRALAKRNLTIVNAVAPGTEIDMDGELPEDEVKAOMLQDIFL-ARLGQPEEVAKAVR		223
Qy	239	AIITEN--PLINGEIVFLDCAIRK		259
Db	224	FLASDDASVLTGQTHVNGGMV		246

Search completed: June 23, 2003, 14:32:47  
Job time : 33.6667 secs





Db 8 AVITGMXXRXRAGRPARRRRL---ARSALFDLMDKGAAGVAGIADKARYFNVNS 63  
 Qy 67 SEKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKGOTHTLEDFQVLDVNLMTG 126  
 Db 64 DEAAVTAAIDQAHDFLEGLVAVNMCAGIILGAGRY--LGKGPMPPLAGFGCTVAVNLVGSF 121  
 Qy 127 NVIRLVAGEMGQNPDDGGQGVIIINTASVAAPFEGVGAAYASAKSGIYGMPLIARDL 186  
 Db 122 NVAKAANRMQHNAGTGERGVYIINTASIAAYEGIGGAAYASAKSGVSMPLPMAREL 181  
 Qy 187 APGIRVWTIAPGLFEGTPLLSTPEKY 213  
 Db 182 SREGIRVWTIAPGFVTPMDGMEAV 208

## RESULT 18

OSHL1 PRELIMINARY; PRT; 246 AA.  
 ID 08XHL1  
 AC 08XHL1  
 DT 01-MAR-2002 (TRENBLREL. 20, Created)  
 DT 01-MAR-2002 (TRENBLREL. 21, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier-protein] reductase.  
 GN FABG OR CPE1070.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
 OC Clostridiales; Clostridiaceae; Clostridium.  
 NCBI\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=13 / TYPE A;  
 RX PubMed=11792842;  
 RA Shintzu T., Ohtani K., Hirakawa H., Oshima K., Yamashita A.,  
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;  
 RA "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 DR EMBL; AF003189; BAB8076.1;  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short.1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT.1.  
 KW Complete proteome.  
 SQ SEQUENCE 246 AA; 26267 MW; CD90B6C650EC817 CRC64;

Query Match 28.5%; Score 373.5; DB 16; Length 246;  
 Best Local Similarity 35.8%; Pred. No. 1.9e-18;  
 Matches 93; Conservative 47; Mismatches 97; Indels 23; Gaps 7;

Qy 8 VGVIAVITGAGSLGATRELVGQASAVLDDPNSGGEQAARKL-----GNCCVAP 62  
 Db 2 LDKDAIIVGGTRIGRATLALADOGAN-IYINRNSDKAEELKALIEKGVVIVK 60  
 Qy 63 ADVTSKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKGOTHTLEDFQVLDVNL 122  
 Db 61 CQISNEDSKNLMDCKEVEFKIDILVNNAGITKTLIRME-----EDDNVLDVNL 114  
 Qy 123 MGTENVIRLVAGEMQNPDDGGQGVIIINTASVAAPFEGVGAAYASAKSGIYGMPL 181  
 Db 115 KGTENCARHSAIMK-----QRFKILNMTSVVGINAGNVYASAKSGVIGLTKS 167  
 Qy 182 IARDLAPIGIRVWTIAPGLFEGTPLLSTPEKYCNFLASQVPPSPRLGDPAEVAHLVQAI 241  
 Db 168 LAKELGSRGITVAVNAPGFINTDMTASLEKYEKESKNIPL-KRLGDEVDVAVNLVGSF 226  
 Qy 242 ENP--FLNGEYIRLDGAIK 259  
 Db 227 SDANVITGVYINVDGMVA 246

RESULT 19  
 Q99YD6 PRELIMINARY; PRT; 244 AA.  
 ID Q99YD6

AC Q99YD6;  
 DT 01-JUN-2001 (TRENBLREL. 17, Created)  
 DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE Putative beta-ketacyl-ACP reductase (EC 1.1.1.100).  
 GN FABG OR SPY1749.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Streptococcaceae; Streptococcus.  
 NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;  
 RX MEDLINE=21192684; PubMed=11296296;  
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lal H.S., Lin S.P.,  
 RA Qian Y., Jia H.G., Nejar F.Z., Ren Q., Zhu H., Song L., White J.,  
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin K.;  
 RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes."  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 DR EMBL; AE006603; AAK34493.1;  
 DR HSP; P50162; IAE1.  
 DR InterPro; IPR002198; ADH\_short.  
 DR InterPro; IPR001092; HLH\_basic.  
 DR Pfam; PF00106; adh\_short.1.  
 DR PRINTS; PR01608; BACINVASINC.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT.1.  
 DR PROSITE; PS00036; HELIX\_LOOP\_HELIX; UNKNOWN\_1.  
 KW Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 244 AA; 26002 MW; 67ECE23670D4065 CRC64;

Query Match 27.2%; Score 355.5; DB 16; Length 244;  
 Best Local Similarity 35.4%; Pred. No. 3.4e-17;  
 Matches 92; Conservative 41; Mismatches 102; Indels 25; Gaps 5;

Qy 8 VGVIAVITGAGSLGATRELVGQASAVLDDPNSGGEQAARKL-----GNCCVAP 60  
 Db 3 IKGRNIRITGSTRIGISLMAHQFASLEAVNL-----NGSASIEELVASTDYGVVY 57  
 Qy 61 APADVSEKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKGOTHTLEDFQVLDV 120  
 Db 58 ISGVDSASAEKKRVNVAISLSIGSIDVYNNAGIT-----NDKIMLKMEEDFERVTKI 111  
 Qy 121 NMGTFENVIRLVAGEMQNPDDGGQGVIIINTASVAAPFEGVGAAYASAKSGIYGMPL 180  
 Db 112 NLGAFNMGTQSVL-----KPMIKARQALINSSVGLTGNIGQANVYASAKSGIMGTG 165  
 Qy 181 PIARDLAPIGIRVWTIAPGLFEGTPLLSTPEKYCNFLASQVPPSPRLGDPAEVAHLVQAI 240  
 Db 166 SVAREVAAARNCVAVNAPGFIESDMTGVLEKMEQLSQIPM-KRLGKQGEVAVNLVGSF 224  
 Qy 241 IENPFLNGEYIRLDGAIK 260  
 Db 225 VEODYITGVYINVDGMTQ 244

RESULT 20  
 Q9HW15 PRELIMINARY; PRT; 252 AA.  
 ID Q9HW15  
 AC Q9HW15  
 DT 01-MAR-2001 (TRENBLREL. 16, Created)  
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)  
 DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)  
 DE Probable short-chain dehydrogenase.  
 GN PA4389.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 NCBI\_TaxID=287;  
 RN [1]

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ID 08T2L7 PRELIMINARY: PRT: 264 AA.  
AC 08T2L7;  
DT 01-JUN-2002 (TREMblrel. 21, Created)  
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE 3-hydroxyacyl-CoA dehydrogenase type II.  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RA Gloeckner G., Eichinger L., Szafarski K., Pachbat J., Dear P.,  
RA Lehmann R., Baumgart C., Parra G., April J.F., Guido R., Kumpf K.,  
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,  
RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.",  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AC115594; AAL92306.1; -  
SQ SEQUENCE 264 AA; 28795 MW; 3C0007DA1309F294 CRC64;  
Query Match 46.1%; Score 603.5; DB 5; Length 264;  
Best Local Similarity 48.8%; Pred. No. 2,6e-34;  
Matches 127; Conservative 46; Mismatches 78; Indels 9; Gaps 5;  
QY 8 VKGLAVITGASGLIATAEPLVGGASAVLDDLPNSGGEAOKKLGNNCFAPADVTSEKD 66  
DB 3 INGTFFVVTGGASGLIETSRHLISGANIFIMDMNEENGRKYVEELGSKTFSSVDIT 62  
QY 67 SEXVOALALAKKGFPRVAVNACAGIYASAKYNNLKKGOTLLEDFQVLDVNLNGTF 126  
DB 63 LEDSVKLSLEHCKLKEFHEHGVINACGAAAGVIRK RDGQVHPLDFTFVAVVNLIGTF 121  
QY 127 NVIRLVAGEM-GONEPD--OGG---ORGYIINTASYAAFEQVGAAYASAGGIYGMT 179  
DB 122 NVIRLVADIIHNOQPSKDGEEEEKGVFIMTASYAAFEQVGAAYASAGGIYGMT 181  
QY 180 LPIRLDAPIGIRMTIAPGLFGLTSLPEKCNFLASOVPPSRIGDPAEYAHLYQA 239  
DB 182 LPMAREFTTKIRINTIAPGFTFETPVMELPQAIKINSIESIPPSMGKPKERAFICQH 241  
QY 240 IITENPFLNGEYIRLDGAIRM 259  
DB 242 LIENTYINGEYIRLDGALRL 261  
RESULT 16  
Q9ABU6 PRELIMINARY: PRT: 260 AA.  
AC Q9ABU6;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
DE 3-hydroxyacyl-CoA dehydrogenase.  
GN CC0124.  
OS Caulobacter crescentus.  
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;  
CC Caulobacter.  
OX NCBI\_TaxID=155892;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 19089 / CB15;  
RA MEDLINE=21173698; PubMed=11259647;  
RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
RA Potocka I., Nelson R.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
RA Dewoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
RA Kolonay J.F., Smit J., Craven M.B., Khouli H., Shetty J., Berry K.,  
RA Ulfendack J., Tran K., Wolf A., Yamathavan J., Ermolaeva M., White O.,  
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
RT "Complete genome sequence of Caulobacter crescentus.",  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
(SDR) FAMILY

DR EMBL: AE005687; AAK22111.1; -  
DR HSSP: O70351; IE3S.  
DR TIGR: CC0124; -  
DR InterPro: IPR002198; ADH\_Short.  
DR InterPro: IPR00205; NAD\_binding.  
DR Pfam: PF00106; adh\_Short; 1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KW Oxidoreductase; Complete proteome.  
SQ SEQUENCE 260 AA; 27075 MW; 7DC145D069C89029 CRC64;  
Query Match 45.5%; Score 595; DB 16; Length 260;  
Best Local Similarity 51.0%; Pred. No. 9,8e-34;  
Matches 130; Conservative 30; Mismatches 89; Indels 6; Gaps 2;  
QY 11 LVAVTGASGLIATAEPLVGGASAVLDDLPNSGGEAOKKLGNNCFAPADVTSEKD 70  
DB 7 VAAVVTGASGLIETSRHLISGANIFIMDMNEENGRKYVEELGSKTFSSVDIT 64  
QY 71 VOTALALAKKGFPRVAVNACAGIYASAKYNNLKKGOTLLEDFQVLDVNLNGTF 126  
DB 65 VDAGEFEKRAAAGQERILVNCAGTGNARKTASRDKATGETHFPLDADRILQINLVGTF 124  
QY 127 NVIRLVAGEMGONEPDGQSGVINTASYAAFEQVGAAYASAGGIYGMTLPIARDL 186  
DB 125 RCIASAKGMDDLEPLDEGERAIYNTASVAAEDQMGAAYASAGGIYGMTLPIARDL 184  
QY 187 APIGRVMTIAPGLFGLTSLPEKCNFLASQVPPFSRIGDPAEYAHLYQAIIENPFL 246  
DB 185 MGEGRIVNTILPGIFNTPLMNNAPAYNAGLAASVFPFRUGHEPEYAOALATMTTCGF 244  
QY 247 NGEVIRLDGAIRMP 261  
DB 245 NGEVDVLDGIRNAP 259  
RESULT 17  
Q93SJ3 PRELIMINARY: PRT: 443 AA.  
AC Q93SJ3;  
DT 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE USC5-2P.  
OS Myxococcus xanthus.  
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;  
CC Myxococcales; Cystobacteriineae; Myxococcaceae; Myxococcus.  
OX NCBI\_TaxID=34;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CECT 422;  
RA Poza M., Siefert C., Villa T.G.;  
RT "Clone USC5 from Myxococcus xanthus CECT 422 strain.",  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
(SDR) FAMILY.  
CC EMBL: AY033405; AAK49009.1; -  
DR InterPro: IPR002198; ADH\_Short.  
DR InterPro: IPR001059; EF-P.  
DR InterPro: IPR001092; HLH\_Basic.  
DR Pfam: PF00106; adh\_Short; 1.  
DR Pfam: PF01132; BFP; 1.  
DR PROSITE: PS00061; ADH\_SHORT; UNKNOWN\_1.  
DR PROSITE: PS00038; HELIX\_LOOP\_HELIX; UNKNOWN\_1.  
KW Oxidoreductase.  
SQ SEQUENCE 443 AA; 47589 MW; 214157EDFD5FA20 CRC64;  
Query Match 29.5%; Score 386; DB 2; Length 443;  
Best Local Similarity 46.4%; Pred. No. 5,3e-19;  
Matches 96; Conservative 29; Mismatches 70; Indels 12; Gaps 5;  
QY 13 AVITG---GASGLIATAEPLVGGASAVLDDLPNSGGEAOKKLGNNCFAPADVTSEKD 66  
DB 13 AVITG---GASGLIATAEPLVGGASAVLDDLPNSGGEAOKKLGNNCFAPADVTSEKD 66

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Db 187 MTIACGIEETPMACMGTEEBRSLAAGVPPPRGROEVAALARIHIIENSMNGEYIRL 246  
Qy 254 DGAIRM 259  
Db 247 DGAIRM 252

RESULT 13

Q80F12 PRELIMINARY: PRT: 257 AA.  
ID Q80F12  
AC Q80F12  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)  
DE 3-hydroxyacyl-CoA dehydrogenase type II.  
GN ATU1415 OR AGR\_C\_2615.  
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_Taxid=176299;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21608550; PubMed=11743193;  
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,  
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
RA Kityavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,  
RA Raymond C., Rouse G., Seshphimachak C., Wu Z., Romero P., Gordon D.,  
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry M.,  
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
RA Nester E.W.;  
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
RT C58.";  
RT Science 294:2317-2323(2001).

RL Science 294:2317-2323(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21608551; PubMed=11743194;  
RA Goodner B., Hinkle G., Gestung S., Miller N., Blanchard M.,  
RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
RA Houmel K., Gordon J., Vaudin M., Tatchouk O., Epp A., Liu F.,  
RA Wolman C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,  
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,  
RA Cielo C., Slater S.;  
RT "Genome sequence of the plant pathogen and biotechnology agent  
RT Agrobacterium tumefaciens C58.";  
RL Science 294:2323-2328(2001).  
DR EMBL: AE009102; AAL42421.1;  
DR EMBL: AE008067; AAK87207.1;  
KW Complete proteome.  
SQ SEQUENCE 257 AA; 26622 MW; FF74A61FFC4B2B5C CRC64;

Query Match 49.0%; Score 642; DB 16; Length 257;

Best Local Similarity 51.7%; Pred. No. 5.4e-37;  
Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

Qy 7 SVKGLVAVITGGASGLTATRLVGGASAVLLDLPSNGSGEAKKKGNCCVPAPADVT 66  
Db 2 NIEGAGALVTGAASGIGAAVAVARMLAARGAAVTIIFRNGEAGKRLAAEIGKAV--QGCVT 59  
Qy 67 SEKDVOGATALAKGKRGVDAVAVACAGIYVASKTYNKKGGHTIEDFORVLDVLMKTF 126  
Db 60 SBDADAAATKVAASAGGRLITVNCAGITAGRT--IGREGQPLGDFEYIRVNLITF 117  
Qy 127 NVIRLVAAGMGNEPDG---GQNGVITNTASVAAFEGQQAAYASAKGIVGMLPI 182  
Db 118 NMRRLAAAHVAERDEDEGDSQDNGVIVNTASVAFEGQIGQAAYASAKGIVSLADPA 177  
Qy 183 ARDLAPLIGIRVMTIAGLFGTPLTSLPKVCNPLASQVPPSRIGDPAEVAHVAHQVATIE 242  
Db 178 ARRLAFRIKRVNTVAAGIIFLTPLLOGIIPQVQESLAGQIIPHSRIGDPAEFAFDYRFLIE 237

Qy 243 NEPLNGEYIRLDGAIMOP 261  
Db 238 NDYNGEYIRLDGAIMOP 256

RESULT 14

Q9DCX5 PRELIMINARY: PRT: 126 AA.  
ID Q9DCX5  
AC Q9DCX5;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)  
DE Hydroxycyco-enzyme A dehydrogenase, type II.  
GN HSD17B10 OR HADH2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fritschmann W., Gaasterland T., Gissi C., King B., Kochiya H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikiado I., Pesole G., Quackenbush J.,  
RA Schirni L.M., Staubl F., Suzuki R., Tomita M., Wagner T., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,  
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weiss C., Whitaker C., Wilmberg L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).

CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
(SDR) FAMILY.  
DR EMBL: AK002368; BAB22046.1;  
DR HSSP: O70351; 1E6W.  
DR MGD: MGI:1333871; Hsdl7b10.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short.1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 126 AA; 13265 MW; 78FFB6D441B9989D CRC64;

Query Match 46.4%; Score 607; DB 11; Length 126;

Best Local Similarity 95.2%; Pred. No. 6.2e-35;  
Matches 120; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 136 MGNEPDGQGGQGVITNTASVAAFEGQQAAYASAKGIVGMLPIARDLAPIGIRVMT 195  
Db 1 MGNEPDGQGGQGVITNTASVAAFEGQQAAYASAKGIVGMLPIARDLAPIGIRVMT 60  
Qy 196 IARGLEGTPLTSLPKVCNPLASQVPPSRIGDPAEVAHVAHQVATIEENPLNGEYIRLDG 255  
Db 61 IARGLEGTPLTSLPKVCNPLASQVPPSRIGDPAEVAHVAHQVATIEENPLNGEYIRLDG 120  
Qy 256 AIRMOP 261  
Db 121 AIRMOP 126  
RESULT 15  
0812L7





NCBI\_TaxID=305;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=GM1000;  
 RA MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
 RA Ariat M., Billault A., Brotlier P., Camus J.C., Catolico L.,  
 RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,  
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,  
 RA Siguer P., Thebaud P., Whalen M., Winkler P., Levy M.,  
 RA Weissbach J., Boucher C.A.;  
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*";  
 RL Nature 415:497-502(2002).  
 DR EMBL; AL646070; CAD16241.1; -  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short.1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 252 AA; 25642 MW; D6BEACDA99179DF CRC64;  
 Query Match 52.7%; Score 689.5; DB 16; Length 252;  
 Best local similarity 57.1%; Pred. No. 2,7e-40;  
 Matches 145; Conservative 33; Mismatches 71; Indels 5; Gaps 3;  
 QY 8 VKGLAVITGASGLGATLAEELVGGASAVLDPNMSGGEAOKKIGNNCVFAPADYTS 67  
 Db 3 IRDVFVITVGASGIGAGITPRALAEAGKVVIALDLNAGAAALAEIGGR--EVRCVSS 60  
 QY 68 EKDQVTLALAKKGFGRVDVAVNCAGTAVASKTYNLKKGTHTEDEFORVLDVNLMTGFN 127  
 Db 61 EADGAAVQAAFT-SIGALAGLVNCAGITAPASRT--VKGAGHPIDQPARVININILIGTFN 117  
 QY 128 VIRLVAGMGQNEPDGQGVVINTASVAAFEGQVQAAYASAKSGITGNTPIADLA 187  
 Db 118 MIRLAATAMTANAPAGGEGVINTASVAAFDQIGQAAYAAKSGVAVMTLAIADLS 177  
 QY 188 PIGRVMTIAGLGTPLTSLPERKVCNFLASQVFPSPRLGDPPEYAHVVOAITENPFLN 247  
 Db 178 RDGIWMTIAPGILETPELTPSLPERKVCNFLASQVFPSPRLGDPPEYAHVVOAITENPFLN 237  
 QY 248 GEVIRLDGAIRMOP 261  
 Db 238 GETIRLDGAIRMOP 251  
 RESULT 9  
 ID 006544 PRELIMINARY; PRT; 250 AA.  
 AC 006544;  
 DT 01-JUL-1997 (TREMblrel. 04, Created)  
 DT 01-JUL-1997 (TREMblrel. 04, last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, last annotation update)  
 DE Oxidoreductase, short-chain dehydrogenase/reductase family.  
 GN RV1144 OR MTC165.11 OR MT1177.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriales; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RA MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Baahm D., Brown D., Chillingworth T., Connor R.,  
 RA Davies K., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,  
 RA Hornby T., Jorgels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream A.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Stalston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the  
 complete genome sequence."

RL Nature 393:537-544(1998).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / OSHKOSH;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri E., Gill J., Mikula A.,  
 RA Bisht W.;  
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and  
 laboratory strains";  
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; Z55584; CAB09032.1; -  
 DR EMBL; AE006996; AAK45436.1; -  
 DR HSSP; 070351; 1E3S.  
 DR TIGR; MT1177; -  
 DR Tuberculosis; RV1144; -  
 DR InterPro: IPR002198; ADH\_short.  
 DR InterPro: IPR00205; NAD-binding.  
 DR Pfam; PF00106; adh\_short.1.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 250 AA; 25787 MW; 123A1005A12BD6B6 CRC64;  
 Query Match 51.3%; Score 671.5; DB 16; Length 250;  
 Best local similarity 60.1%; Pred. No. 4,7e-39;  
 Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;  
 QY 9 KGLAVITGASGLGATLAEELVGGASAVLDPNMSGGEAOKKIGNNCVFAPADYTS 68  
 Db 4 KDAVAVITGASGLGATLAEELVGGASAVLDPNMSGGEAOKKIGNNCVFAPADYTS 60  
 QY 69 KDQVTLALAKKGFGRVDVAVNCAGTAVASKTYNLKKGTHTEDEFORVLDVNLMTGFN 128  
 Db 61 AAVSNALIELA-DLGLPVRVYVNCAGTGNARV--LSRDGFTPLAARKIYDNLVGTENV 117  
 QY 129 IRLVAGMGQNEPDGQGVVINTASVAAFEGQVQAAYASAKSGITGNTPIADLA 188  
 Db 118 IRLGAEIRAKTER-IGERGVVINTASVAAFDQIGQAAYAAKSGVAVMTLAIADLS 176  
 QY 189 IGRVMTIAGLGTPLTSLPERKVCNFLASQVFPSPRLGDPPEYAHVVOAITENPFLN 248  
 Db 177 KLIRVMTIAPGLTPELTPSLPERKVCNFLASQVFPSPRLGDPPEYAHVVOAITENPFLN 236  
 QY 249 EVIRLDGAIRMOP 261  
 Db 237 EVIRLDGAIRMOP 249  
 RESULT 10  
 ID 092YS1 PRELIMINARY; PRT; 255 AA.  
 AC 092YS1;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, last annotation update)  
 DE Probable.  
 GN RA0792 OR SMA1452.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Rhizobium pSymb (megaplasmid 1).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RA MEDLINE=21396509; PubMed=11481432;  
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,  
 RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,  
 RA Gurjani M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,  
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,  
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;  
 RT "Nucleotide sequence and predicted functions of the entire

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OY 123 MGFENVIRLVAGEMGNEPDGORGVIINTASVAAFEGGVGQAAYSASKGIVGMLPI 182
    :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 120 LGTFNVIRHGVNLMGEHEKNDANGORGVIINTASVAAFDGTGQASYSASKGIVGMLPI 179
OY 183 ARDLAPGIRVMTIAPGLFTPLITSLEPEVCNFIASQVFPFRLDPAEYALVQALIE 242
    :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 180 ARDFAGGIRFNTIAPGLMDIPLISLPERKSFIAOLIPFRLGHPHEGALVQHIE 239
OY 243 NPFLNGEIVRLDGAIRM 259
    :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 240 NGVINGETIRFDGALRM 256

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## RESULT 6

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O910T0 PRELIMINARY: PRT: 255 AA.
AC 0910T0:
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Probable short-chain dehydrogenase.
GN PA2554.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
CC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stoyer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lam R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1. SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
    (SDR) FAMILY.
DR EMBL: AE004683; AAC05942.1; -
DR HSSP: C70351; 1B3S.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PRO0080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 255 AA; 26426 MW; EB8FF28712D2936D CRC64;

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Query Match 55.0%; Score 720; DB 16; Length 255;  
 Best Local Similarity 57.5%; Pred. No. 2,1e-42;  
 Matches 145; Conservative 39; Mismatches 66; Indels 2; Gaps 1;

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OY 8 VKGLAVITGASGLATAERLVGOGASAVLLDLPNSGGEQAOKLGNCCVFAPADYTS 67
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 IENRFVITGSGSGGLATAKLVGGGKVVLDINAEGAKAKAELGAQAREVADIAS 62
OY 68 EKDVOITALAKGKGRVDVAVNCAGIAVASTYLLKKGGHTLDEDFORVLDVNMGTEN 127
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 EADGRQVAAALAEAGLGLANLCAGVAPAEKV--LGRNGJHALDSFRVIDINLVGSFN 120
OY 128 VIRLVAGEMGNEPDGORGVIINTASVAAFEGGVGQAAYSASKGIVGMLPIARDLA 187
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 MRLAAEMASQGPDEGSRGIVTASAAFDGILGAAYSASKSGVGMPLIARELA 180
OY 188 PIGIRVMTIAPGLFTPLITSLEPEVCNFIASQVFPFRLDPAEYALVQALIEPFLN 247
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 RGIRVMTIAPGLFTPLITSLEPEVCNFIASQVFPFRLDPAEYALVQALIEPFLN 240
OY 248 GEVIRLDGAIRM 259
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 GEVIRLDGAIRM 252

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## RESULT 7

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O8YBSO PRELIMINARY: PRT: 255 AA.
ID O8YBSO
AC O8YBSO:
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100).
GN BMEI10816.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL: AE009715; AL54058.1; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PRO0080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 255 AA; 26263 MW; 5CF61D4B37F6B730 CRC64;

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Query Match 54.3%; Score 711; DB 16; Length 255;  
 Best Local Similarity 57.1%; Pred. No. 9e-42;  
 Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

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OY 8 VKGLAVITGASGLATAERLVGOGASAVLLDLPNSGGEQAOKLGNCCVFAPADYTS 67
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 IENRFVITGSGSGGLATAKLVGGGKVVLDINAEGAKAKAELGAQAREVADIAS 62
OY 68 EKDVOITALAKGKGRVDVAVNCAGIAVASTYLLKKGGHTLDEDFORVLDVNMGTEN 127
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 DTGKAAITAAIAEFNSHIDVAVNCAGVAPAEKV--LGRGAHLLEFTTTSINLIGTFN 120
OY 128 VIRLVAGEMGNEPDGORGVIINTASVAAFEGGVGQAAYSASKGIVGMLPIARDLA 187
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 MRLAAEMASQGPDEGSRGIVTASAAFDGILGAAYSASKSGVGMPLIARELA 180
OY 188 PIGIRVMTIAPGLFTPLITSLEPEVCNFIASQVFPFRLDPAEYALVQALIEPFLN 247
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 RHGIRVMTIAPGLFTPLITSLEPEVCNFIASQVFPFRLDPAEYALVQALIEPFLN 240
OY 248 GEVIRLDGAIRM 259
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 GEVIRLDGAIRM 252

```

## RESULT 8

```

O8XWEO PRELIMINARY: PRT: 252 AA.
ID O8XWEO
AC O8XWEO:
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Probable 3-hydroxyacyl-CoA dehydrogenase type II oxidoreductase
DE protein (EC 1.1.1.35).
GN RSC2534 OR RS05766.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.

```

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,  
 RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,  
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RA "Functional annotation of a full-length mouse cDNA collection.",  
 RT Nature 409:685-690(2001)  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 DR EMBL: AK013340; BAB28800.1; -.  
 DR HSSP: O70351; 1B6W.  
 DR MGD: MGI:1333871; Hsd17b10.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Oxidoreductase.  
 SQ SEQUENCE 261 AA; 27273 MW; F36CD19GCFEEFAF CRC64;

Query Match 88.1%; Score 1153; DB 11; Length 261;  
 Best Local Similarity 87.4%; Pred. No. 2.4e-72;  
 Matches 228; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

OY 1 MAACRSYKGLVAVITGGASGLGATATRLVGGASAVLLDLPNSGGEQAQKLNVCVF 60  
 DB 1 MAASVYKGLVAVITGGASGLGATATRLVGGASAVLLDLPNSGGEQAQKLNVCVF 60  
 OY 61 APADYSEKDVOTATLALAKGKRGVAVVAVNAGIYVASKTYNLKKGQTHTEDEFORVLDV 120  
 DB 61 APANTSEKELQALTLAKKEGFRIDVAVNAGIYVAKTYHKKKHTHLEDEQRVAVN 120  
 OY 121 NMGTFNVIRLVAGMGONPDQGGQGVYIINTASVAAFEGVGOAAYSASKGIVGML 180  
 DB 121 NLIGTFNVIRLVAGMGONPDQGGQGVYIINTASVAAFEGVGOAAYSASKGIVGML 180  
 OY 181 PIARLAPLPIGIRVMTIAPGLTPTPLTSLPEKVCNFIASOYFEPRLDPAEYAHLYQAI 240  
 DB 181 PIARLAPLPIGIRVMTIAPGLTPTPLTSLPEKVCNFIASOYFEPRLDPAEYAHLYQAI 240  
 OY 241 IENPFLNGEVIRLDGAIKMP 261  
 DB 241 IENPFLNGEVIRLDGAIKMP 261  
 RESULT 4  
 ID 08TCV9 PRELIMINARY; PRT; 196 AA.  
 AC 08TCV9;  
 DT 01-JUN-2002 (TREMblrel. 21, Created)  
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Endoplasmic reticulum-associated amyloid beta peptide-binding protein  
 DE (Fragment).  
 GN ERAB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Deininger M.H., Meyerman R., Schluesselner H.J.;  
 RT "Expression, release and induction of endoplasmic reticulum-associated  
 RT amyloid beta-binding protein in brain disease."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY092415; AAM18189.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 196  
 SQ SEQUENCE 196 AA; 20581 MW; 2400DE14966BAA6A CRC64;

Query Match 75.9%; Score 993; DB 4; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 2e-61;  
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 AKRLGNVCYAPADYSEKDVOTATLALAKGKRGVAVVAVNAGIYVASKTYNLKKGQTH 110  
 DB 1 AKRLGNVCYAPADYSEKDVOTATLALAKGKRGVAVVAVNAGIYVASKTYNLKKGQTH 60  
 OY 111 LEDFORVLDVNLMTGNTVIRLVAGMGONPDQGGQGVYIINTASVAAFEGVGOAAYS 170  
 DB 61 LEDFORVLDVNLMTGNTVIRLVAGMGONPDQGGQGVYIINTASVAAFEGVGOAAYS 120  
 OY 171 SKGIVGMLPIARLAPLPIGIRVMTIAPGLTPTPLTSLPEKVCNFIASOYFEPRLD 230  
 DB 121 SKGIVGMLPIARLAPLPIGIRVMTIAPGLTPTPLTSLPEKVCNFIASOYFEPRLD 180  
 OY 231 AEYAHLYQAIENPFL 246  
 DB 181 AEYAHLYQAIENPFL 196

RESULT 5  
 ID 019102 PRELIMINARY; PRT; 258 AA.  
 AC 019102;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Probable 3-hydroxacyl-CoA dehydrogenase f0164.2 type II (EC 1.1.1.35)  
 DE (Type II HADH).  
 GN F0164.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peliorderinae; Caenorhabditis.  
 OX NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Harris B.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA +  
 CC NADH.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC FAMILY (SDR).  
 CC EMBL: Z68341; CA92764.1; -.  
 DR HSSP: O70351; 1B6W.  
 DR WormPep: F0164.2; CE03127.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 KW Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.  
 FT ACCT SITE 11 36 NAD (BY SIMILARITY).  
 FT ACCT SITE 165 165 BY SIMILARITY.  
 SQ SEQUENCE 258 AA; 27143 MW; 86BF2568EE6902B3 CRC64;

Query Match 57.1%; Score 748; DB 5; Length 258;  
 Best Local Similarity 59.9%; Pred. No. 2.5e-44;  
 Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;

OY 3 AACRSYKGLVAVITGGASGLGATATRLVGGASAVLLDLPNSGGEQAQKLNVCYAP 62  
 DB 2 SALRSTKGLVAVITGGASGLGATATRLVGGASAVLLDLPNSGGEQAQKLNVCYAP 59  
 OY 63 ADVTSSEKDVOTATLALAKGKRGVAVVAVNAGIYVASKTYNLKKGQTHTEDEFORVLDV 122  
 DB 60 ASVTSEEVRAFAKVAEYGRIDLAVNAGIYVAFKLYSVQKKKHVDFFKIRQITIDV 119

90 285.5 21.8 254 16 09RT26  
91 285 21.8 255 16 09PCQ2  
92 284.5 21.7 246 2 09E519  
93 284.5 21.7 257 16 09WYD3  
94 283.5 21.7 253 16 09CH41  
95 283.5 21.7 256 17 08WT5  
96 283 21.6 252 16 092PP0  
97 283 21.6 275 16 09K4H0  
98 282.5 21.6 272 16 099RG1  
99 282.5 21.6 521 16 09A7A9  
100 282 21.5 306 10 091W34

## ALIGNMENTS

RESULT 1  
ID 096HD5 PRELIMINARY; PRT; 252 AA.

AC 096HD5:  
DT 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
DE Similar to hydroxyacyl-coenzyme A dehydrogenase, type II.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
CX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
(SDR) FAMILY.  
CC EMBL: BC008708; AA08708.1; -  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short; 1.  
DR PROSITE: PS00061; ADH\_SHORT; UNKNOWN\_1.  
KW Oxidoreductase.  
SQ SEQUENCE 252 AA; 25984 MW; F36B871070CE872D CRC64;

Query Match 95.5%; Score 1250.5; DB 4; Length 252;  
Best Local Similarity 96.6%; Pred. No. 4.1e-79;

Matches 252; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 1 MAACRSYKGLVAIVTGGASGLGLATAEVLVGOGASAVLIDLPSNGSGRAQAKKLNQVF 60  
DB 1 MAACRSYKGLVAIVTGGASGLGLATAEVLVGOGASAVLIDLPSNGSGRAQAKKLNQVF 60  
QY 61 APADVTSEKDVOTATLAKKFKGRVDVAVNAGIAVASKITNKKGGTHTEDEFORVLDV 120  
DB 61 APADVTSEKDVOTATLAKKFKGRVDVAVNAGIAVASKITNKKGGTHTEDEFORVLDV 120  
QY 121 NLMGTFNIVRLVAGEMGNEPDGOGRGVITNTASVAEFEGVGQAASASAGIVGWT 180  
DB 121 NLMGTFNIVRLVAGEMGNEPDGOGRGVITNTASVAEFEGVGQAASASAGIVGWT 180  
QY 161 PIARDLAPIGIRVMTAPGIFGTPPLTSLPEKVCNPLASQVPPSPRLGDPAPAYAHVQAI 240  
DB 161 PIARDLAPIGIRVMTAPGIFGTPPLTSLPEKVCNPLASQVPPSPRLGDPAPAYAHVQAI 240  
QY 181 PIARDLAPIGIRVMTAPGIFGTPPLTSLPEKVCNPLASQVPPSPRLGDPAPAYAHVQAI 231  
DB 181 PIARDLAPIGIRVMTAPGIFGTPPLTSLPEKVCNPLASQVPPSPRLGDPAPAYAHVQAI 231  
QY 241 IENPFLNGEVIIRLDGAIKMP 261  
DB 241 IENPFLNGEVIIRLDGAIKMP 261

RESULT 2  
ID 099N15 PRELIMINARY; PRT; 261 AA.  
AC 099N15:  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE Short chain L-3-hydroxyacyl-CoA dehydrogenase.  
GN HSD17B10 OR SCHAD.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21098701; PubMed=1165016;  
RA He X.Y., Mertz G., Chu C.H., Lin D., Yang Y.Z., Mehta P., Schultz H.,  
RA Yang S.Y.;  
RT Molecular cloning, modeling, and localization of rat type 10 17beta-  
hydroxysteroid dehydrogenase.\*;  
RT Mol. Cell. Endocrinol. 171:89-98(2001).  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
(SDR) FAMILY.  
CC EMBL: AF233685; AKL15008.1; -  
DR HSSP: O70351; 1E6W.  
DR MGD: MGI:133871; Hsd17B10.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short; 1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 261 AA; 27273 MW; F371ED8A15FCEFAF CRC64;

Query Match 88.4%; Score 1157; DB 11; Length 261;  
Best Local Similarity 87.7%; Pred. No. 1.3e-72;

Matches 229; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAIVTGGASGLGLATAEVLVGOGASAVLIDLPSNGSGRAQAKKLNQVF 60  
DB 1 MAACRSYKGLVAIVTGGASGLGLATAEVLVGOGASAVLIDLPSNGSGRAQAKKLNQVF 60  
QY 61 APADVTSEKDVOTATLAKKFKGRVDVAVNAGIAVASKITNKKGGTHTEDEFORVLDV 120  
DB 61 APADVTSEKDVOTATLAKKFKGRVDVAVNAGIAVASKITNKKGGTHTEDEFORVLDV 120  
QY 121 NLMGTFNIVRLVAGEMGNEPDGOGRGVITNTASVAEFEGVGQAASASAGIVGWT 180  
DB 121 NLMGTFNIVRLVAGEMGNEPDGOGRGVITNTASVAEFEGVGQAASASAGIVGWT 180  
QY 161 PIARDLAPIGIRVMTAPGIFGTPPLTSLPEKVCNPLASQVPPSPRLGDPAPAYAHVQAI 240  
DB 161 PIARDLAPIGIRVMTAPGIFGTPPLTSLPEKVCNPLASQVPPSPRLGDPAPAYAHVQAI 240  
QY 241 IENPFLNGEVIIRLDGAIKMP 261  
DB 241 IENPFLNGEVIIRLDGAIKMP 261

RESULT 3

ID 09CYT3 PRELIMINARY; PRT; 261 AA.  
AC 09CYT3:  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE Hydroxyacyl-coenzyme A dehydrogenase, type II.  
GN HSD17B10 OR HADH2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CS7BL/6J; TISSUE=EMBRYO;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:22:37 ; Search time 31.6667 Seconds

(without alignments)  
1698.262 Million cell updates/sec

Title: US-09-931-186-8

Perfect score: 1309  
Sequence: 1 MAACRSVKGLVAVITGAS.....ENPFNGEVLRLDGAIRMQP 261

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

SPREMBL.21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_plant:\*  
10: sp\_protist:\*  
11: sp\_rotent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeal:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1250.5	95.5	252	4	Q96HDS homo sapien
2	1157	88.4	261	11	Q99N15 mus musculu
3	1153	88.1	261	11	Q9CYT3 mus musculu
4	993	75.9	196	4	Q8RCV9 mus sapien
5	748	57.1	258	5	Q19102 caenorhabdi
6	720	53.0	255	16	Q19100 pseudomonas
7	711	54.3	255	16	Q8YB50 bruceella me
8	689.5	52.7	252	16	Q8YB50 bruceella me
9	671.5	51.3	250	16	Q06544 mycobacteri
10	670	51.0	255	16	Q92YS1 rhizobium m
11	667	51.0	253	16	Q98HM4 rhizobium m
12	662	49.8	255	2	Q9AHY1 pseudomonas
13	642	49.0	257	16	Q9AHY1 pseudomonas
14	607	46.4	126	11	Q8DFI2 agrobacteri
15	603.5	46.1	264	5	Q8DCX5 mus musculu
					Q8C17 dicyosteli

17	386	29.5	443	2	Q93S3J3
18	373.5	28.5	246	16	Q8XJH1
19	355.5	27.2	244	16	Q99YD6
20	355	27.1	252	16	Q9HW15
21	343.5	26.2	249	16	Q97DA6
22	337.5	25.8	247	16	Q8R9W0
23	335.5	25.6	297	3	Q42774
24	334.5	25.6	251	16	Q8YV10
25	334.5	25.5	246	16	Q9KA03
26	332	25.4	248	16	Q9K636
27	326.5	24.9	248	2	Q9KJF1
28	325.5	24.9	243	16	Q9FBC3
29	324.5	24.8	243	16	Q9CHP7
30	324.5	24.8	260	16	Q880F8
31	323.5	24.7	260	4	Q96KR9
32	323	24.7	271	10	Q94G09
33	322	24.6	261	13	Q8UUM4
34	322	24.6	262	2	Q9L9F8
35	321	24.5	263	16	Q9KYM4
36	320	24.4	271	10	Q94G10
37	318.5	24.3	261	6	Q8RMM4
38	317.5	24.2	246	2	Q9EX74
39	317	24.2	258	2	Q9FEV0
40	317	24.2	299	17	Q97UK6
41	314.5	24.0	259	16	Q8U616
42	313.5	23.9	240	17	Q9HY54
43	312.5	23.8	313	2	Q93HC0
44	312	23.8	237	4	Q8WTW8
45	311.5	23.8	236	16	Q9AUB2
46	311.5	23.8	296	16	Q9ABX6
47	311	23.8	247	16	Q9EPF6
48	311	23.8	262	16	Q8YD94
49	310	23.6	267	10	P93697
50	309.5	23.6	244	16	Q8ZFT5
51	309	23.6	253	16	Q8U759
52	308.5	23.6	260	17	Q8UB33
53	306	23.4	256	16	Q8ZBQ6
54	303.5	23.2	236	11	Q91VT4
55	303.5	23.2	247	16	Q8Y690
56	303	23.1	248	16	Q8U9B5
57	302.5	23.1	249	2	Q9LBS5
58	302	23.1	263	2	Q9S5E7
59	302	23.1	273	2	Q9F5T1
60	301.5	23.0	247	16	Q92AK1
61	301	23.0	247	2	Q9ZP93
62	300.5	22.9	296	5	Q9XX28
63	300	22.9	250	2	Q56840
64	298	22.8	252	17	Q97UA4
65	296.5	22.7	558	16	Q33339
66	296.5	22.7	235	2	Q8VW75
67	296	22.6	248	16	Q8TDM1
68	295.5	22.6	254	16	Q92PP8
69	295	22.5	260	16	Q9ZPB1
70	294	22.5	255	17	Q9HQ41
71	294	22.5	265	16	Q9S2E4
72	293.5	22.4	267	2	Q9LBS2
73	291	22.2	255	16	Q8RPG3
74	291	22.2	258	16	Q93DL5
75	291	22.2	315	10	Q945M3
76	291	22.2	320	10	Q93X62
77	290.5	22.2	270	4	Q9URJ3
78	290.5	22.2	270	4	Q9BXP1
79	290	22.2	245	2	Q93HB3
80	290	22.2	272	16	Q8YHE0
81	290	22.2	328	16	Q93X67
82	289.5	22.1	405	16	Q98AS0
83	288	22.0	243	16	Q8RG25
84	287.5	22.0	303	10	Q93CQ0
85	287.5	22.0	303	10	Q9SCU0
86	286.5	21.9	244	16	Q8X815
87	286.5	21.9	245	16	Q8RDP9
88	286.5	21.9	246	2	Q9R8B0
89	286.5	21.9	251	10	Q94Y07
90	286.5	21.9	251	10	Q94Y07

Q93S3J3 myxococcus
Q8XJH1 clostridium
Q99YD6 streptococ
Q9HW15 pseudomonas
Q97DA6 clostridium
Q8R9W0 thermocanaer
Q42774 neurospora
Q8YV10 arabidena sp
Q9KA03 bacillus ha
Q9K636 bacillus ha
Q9KJF1 thauera aro
Q9FBC3 streptococ
Q9CHP7 lactococcus
Q880F8 streptomyc
Q96KR9 homo sapien
Q94G09 cucumis sat
Q8UUM4 oryzias lat
Q9L9F8 streptomyc
Q9KYM4 streptomyc
Q94G10 cucumis sat
Q8RMM4 mecaea mula
Q9EX74 rhodococcus
Q9FEV0 streptomyc
Q97UK6 sulfolobus
Q8U616 agrobacteri
Q9HY54 pyrococcus
Q93HC0 streptomyc
Q8WTW8 homo sapien
Q9AUB2 thauera aro
Q9ABX6 caulobacter
Q9EPF6 xyella fas
Q8YD94 bruceella me
P93697 vigna ungui
Q8ZFT5 yerinia pe
Q8U759 agrobacteri
Q8UB33 pyrococcus
Q8ZBQ6 yerinia pe
Q91VT4 mus musculu
Q8Y690 listeria mo
Q8U9B5 agrobacteri
Q9LBS5 geobacillus
Q9S5E7 streptomyc
Q9F5T1 streptomyc
Q92AK1 listeria in
Q9ZP93 bacillus me
Q9XX28 caenorhabdi
Q56840 xanthobacte
Q97UA4 sulfolobus
Q33339 mycobacteri
Q8VW75 mycobacteri
Q8TDM1 bruceella me
Q92PP8 rhizobium m
Q9ZPB1 streptomyc
Q9HQ41 halobacteri
Q9S2E4 streptomyc
Q9LBS2 leifsonia a
Q8RPG3 thermocanaer
Q93DL5 rhizobium m
Q945M3 brassica na
Q93X62 brassica na
Q9URJ3 homo sapien
Q9BXP1 homo sapien
Q93HB3 streptomyc
Q8YHE0 bruceella me
Q93X67 brassica na
Q98AS0 rhizobium l
Q8RG25 fusbocacteri
Q93CQ0 arabidopsi
Q9SCU0 arabidopsi
Q8X815 escherichia
Q8RDP9 thermocanaer
Q9R8B0 burkholderi
Q94Y07 burkholderi

Thu Jun 26 06:55:09 2003

us-09-931-186-6.rag

Page 17

QY 129 IRLVAGEMGONEDDGGORGVITINTASVAFEGOVQAAYSASKGIYGMTLPIARDLAP 188  
Db 124 IQAITEGF-----DKLGHGSKIINATISQAGVEGNGLSIXSTKFAVRGLTQYAADLAE 178  
QY 189 IGIRVMTIAPGLFGTPLTSLPEKVCNFLASQVFP-----SRIGDPAEYA 234  
Db 179 KNTIVNAFAPGIYETPMMKGIKAEK---LAENNCPMENGWKOFTDQIALKRISKPEDEYA 234  
QY 235 HLYQAI--ENPFLNGEVIRLDCAIR 258  
Db 235 NVVSFLAGSDSDYITGOTIIVDGMR 260

Search completed: June 23, 2003, 14:28:30  
Job time : 41.6667 secs

RESULT 24  
ABP39667 standard; Protein; 263 AA.  
XX ID ABP39667;  
XX AC ABP39667;  
XX DT 24-JUL-2002 (first entry)  
XX DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4512.  
XX DE Staphylococcus epidermidis; open reading frame; ORF, bacterial infection;  
XX DE antibacterial; gene therapy.  
XX OS Staphylococcus epidermidis.  
XX OS US6380370-B1.  
XX PN 30-APR-2002.  
XX PD 13-AUG-1998; 98US-0134001.  
XX PE 14-AUG-1997; 97US-055779P.  
XX PR 08-NOV-1997; 97US-064964P.  
XX PA (GENO-) GENOME THERAPEUTICS CORP.  
XX PI Doucette-Stamm LA, Bush D;  
XX DR WPI: 2002-381255/41.  
XX DR N-PSDB; ABN92212.  
XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis  
XX PS polypeptide, useful for diagnosing and treating bacterial infections -  
XX PS Disclosure: SEQ ID 4512; 267pp; English.  
XX CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading  
XX CC frame (ORF) nucleic acid sequences which encode the amino acid sequences  
XX CC given in ABP35124 to ABP37960. The S. epidermidis sequences have  
XX CC antibacterial activity and can be used in gene therapy. The sequences  
XX CC can also be used in the diagnosis and treatment of bacterial infections,  
XX CC particularly S. epidermidis infections. The sequences can be used to  
XX CC screen for compounds able to interfere with the S. epidermidis life  
XX CC cycle or inhibit S. epidermidis infection.  
XX CC N.B. The sequence data for this patent did not form part of the printed  
XX CC specification, but was obtained in electronic format directly from the  
XX CC USPTO web site.  
XX SO Sequence 263 AA;  
Query Match 22.6%; Score 295; DB 23; Length 263;  
Best Local Similarity 32.3%; Pred. No. 8e-20;  
Matches 86; Conservative 42; Mismatches 104; Indels 34; Gaps 6;  
DB 12 VAVITGASGLGATLAEFLVGGASAVLLDLPNSGGEAQAATL--GNNVFAPADVTSE 68  
11 VAVITGASGLGATLAEFLVGGASAVLLDLPNSGGEAQAATL--GNNVFAPADVTSE 68  
10 VAVITGASGLGATLAEFLVGGASAVLLDLPNSGGEAQAATL--GNNVFAPADVTSE 68  
9 KDVOTATLALAKKGFGRVDVAVNAGIAVASKTYNLKKGOTHTLEDQRVLVDVNLMTFNV 128  
8 KDVOTATLALAKKGFGRVDVAVNAGIAVASKTYNLKKGOTHTLEDQRVLVDVNLMTFNV 128  
71 DOVESVLNQVYEHFEDLNLVNNAGLGPMTPI-----ESVTPDFQNVGVNAGVFWG 124  
129 IRLVAGMEGONPEPDGOGGVINTASVAAFEGVGAAYASAKGIVGMLPTIARDIAP 188  
125 IQALAEQF-----DLGHGKRIINATSGAGVGNAGLSLSTKRAVAGLTVQVARDLAE 179  
189 IGIRVMTAPGLFGFPLITSLPEKVCNLAQVPP-----SRLDGPAEYA 234  
180 KNITVNAFAPGIVETPMKKGIAEK---LAENNQPMEMGKQOTDQIALKRLSKPEDEYA 235  
235 HLVOALIT--ENPFLNGEYIRLDGAIR 258

DB 236 NVVSFLAGSDSDYINGOTIIVDGMR 261  
RESULT 25  
AAG83032 standard; Protein; 262 AA.  
XX ID AAG83032;  
XX AC AAG83032;  
XX DT 03-SEP-2001 (first entry)  
XX DE S. epidermidis open reading frame protein sequence SEQ ID NO:3158.  
XX DE Staphylococcus epidermidis SRI strain; infection; diagnosis;  
XX DE vaccination; endocarditis.  
XX OS Staphylococcus epidermidis.  
XX OS WO200134809-A2.  
XX PN 17-MAY-2001.  
XX PD 09-NOV-2000; 2000MO-US30782.  
XX PE 09-NOV-1999; 99US-0164258.  
XX PR (GLAX ) GLAXO GROUP LTD.  
XX PA Kimmervly WJ;  
XX PI WPI: 2001-316495/33.  
XX DR N-PSDB; AAG83882.  
XX PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
XX PS useful for vaccinating against infections, e.g. endocarditis -  
XX PS Claim 18; Page 833; 2188pp; English.  
XX CC AAG83304 to AAG83970 represent nucleic acids (I) encoding polypeptides  
XX CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis -  
XX CC (I) and (II) can have antibacterial activity and therefore can be used  
XX CC in vaccination. The nucleic acids (I) may be used to produce the  
XX CC S. epidermidis polypeptides (II) via the production of vectors  
XX CC containing them which are used to produce host cells which express the  
XX CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
XX CC used to vaccinate subjects and to raise antibodies against the bacteria.  
XX CC The polypeptides may also be used to assay for other inhibitors of their  
XX CC activity and therefore identify compounds that may be used for the  
XX CC treatment of S. epidermidis infections, e.g. endocarditis. AAG83971 to  
XX CC AAG85090 represent specifically claimed S. epidermidis genomic DNA  
XX CC polynucleotide sequences from the present invention. AAG85091 to  
XX CC AAG85098 represent oligonucleotide sequences and primers which are used  
XX CC in the exemplification of the present invention.  
XX CC N.B. The present invention specifically claims all the polynucleotide  
XX CC sequences given in the sequence listing of the present specification,  
XX CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
XX CC though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,  
XX CC no sequences are present for SEQ ID NO:4455 to 4464.  
XX SO Sequence 262 AA;  
Query Match 22.5%; Score 294; DB 22; Length 262;  
Best Local Similarity 32.3%; Pred. No. 9.9e-20;  
Matches 86; Conservative 41; Mismatches 105; Indels 34; Gaps 6;  
DB 12 VAVITGASGLGATLAEFLVGGASAVLLDLPNSGGEAQAATL--GNNVFAPADVTSE 68  
11 VAVITGASGLGATLAEFLVGGASAVLLDLPNSGGEAQAATL--GNNVFAPADVTSE 68  
10 VAVITGASGLGATLAEFLVGGASAVLLDLPNSGGEAQAATL--GNNVFAPADVTSE 68  
9 KDVOTATLALAKKGFGRVDVAVNAGIAVASKTYNLKKGOTHTLEDQRVLVDVNLMTFNV 128  
8 KDVOTATLALAKKGFGRVDVAVNAGIAVASKTYNLKKGOTHTLEDQRVLVDVNLMTFNV 128  
70 DOVESVLNQVYEHFEDLNLVNNAGLGPMTPI-----ESVTPDFQNVGVNAGVFWG 123



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XX 25-OCT-2000 (first entry)
XX
XX Bacillus megaterium 3-keto-acyl-CoA reductase Phab.
XX
XX Polyydroxyalkanoate; polyydroxybutyrate; transgenic plant; Phab;
XX 3-keto-acyl-CoA reductase.
XX
XX Bacillus megaterium.
XX
XX WO200040730-A1.
XX
XX 13-JUL-2000.
XX
XX 07-JAN-2000; 2000WO-US00364.
XX
XX 07-JAN-1999; 99US-0115592.
XX
XX (UYMA-) UNIV MASSACHUSETTS.
XX
XX Cannon MC, Cannon FC, Mccool GJ, Valentin HE, Gruys KJ;
XX WPI; 2000-532624/48.
XX
XX N-PSDB; AAA50142.
XX
XX New nucleic acid fragment encoding proteins involved in
XX polyydroxyalkanoate (PHA) biosynthesis, useful in the production of
XX transgenic plants or recombinant plant cells which can express PHAs
XX such as polyydroxybutyrate.
XX
XX Claim 85; Page 137-138; 153pp; English.
XX
XX The present sequence is that of Phab, a 3-keto-acyl-CoA-reductase
XX protein of Bacillus megaterium. The sequence was deduced from an
XX open reading frame identified in an isolated 7,916 bp fragment of
XX B. megaterium strain 11561 genomic DNA (see AAA50142). The 7,916 bp
XX DNA fragment includes genes encoding proteins (see AA195743-47)
XX involved in polyydroxyalkanoate (PHA) biosynthesis. Nucleic acids
XX encoding these proteins are useful for creating transgenic plants or
XX recombinant host cells which have the capability of expressing PHAs
XX such as polyydroxybutyrate, polyydroxyvalerate,
XX polyydroxyhexanoate, polyydroxyoctanoate, polyydroxydecanoate or
XX their copolymers. Claimed methods for preparing a PHA involve
XX obtaining a plant or a cell comprising a nucleic acid encoding
XX a 3-keto-acyl-CoA reductase (especially the present sequence), and
XX a nucleic acid encoding a PHA synthase (see AA195747), and growing
XX the plant or cell under conditions suitable for PHA production.
XX
XX
XX Sequence 247 AA;
SQ
Query Match 23.1%; Score 301; DB 21; Length 247;
Best Local Similarity 23.1%; Pred. No. 2e-20;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

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RESULT 23
AAB47459
ID AAB47459 standard; Protein; 267 AA.
XX
XX AAB47459;
AC
XX
XX 13-DEC-2001 (first entry)
XX
XX Levodione reductase.
XX
XX Levodione reductase; homologous subunit; levodione; primer; amplify;
XX (4R,6R)-4-hydroxy-2,2,6-trimethylcyclohexanone; actinol; zeaxanthin;
XX PCR; polymerase chain reaction.
XX
XX Corynebacterium aquaticum.
XX
XX EP1122315-A1.
XX
XX 08-AUG-2001.
XX
XX 29-JAN-2001; 2001EP-0101940.
XX
XX 01-FEB-2000; 2000EP-0101665.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Shimizu S, Wada M;
XX WPI; 2001-551347/62.
XX
XX N-PSDB; AAA43285.
XX
XX New Corynebacterium aquaticum levodione reductase gene, useful for
XX producing levodione reductase for converting levodione to actinol,
XX which is a useful chiral building block of naturally occurring
XX optically active compounds.
XX
XX Claim 3; Page 15-16; 19pp; English.
XX
XX This sequence shows levodione reductase. Levodione reductase has a
XX relative molecular mass of 142-155kD +/- 10kD consisting of four
XX CC homologous subunits each having a molecular mass of 36kD +/- 5kD. This
XX CC enzyme converts levodione to (4R,6R)-4-hydroxy-2,2,6-trimethyl-
XX cyclohexanone (actinol), which is a useful chiral building block of
XX naturally occurring optically active compounds such as zeaxanthin.
XX
XX
XX Sequence 267 AA;
SQ
Query Match 22.8%; Score 297.5; DB 22; Length 267;
Best Local Similarity 31.8%; Pred. No. 4.7e-20;
Matches 84; Conservative 46; Mismatches 97; Indels 37; Gaps 9;

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XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Example 3; Seq ID No 10921; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 245 AA;
XX
XX Query Match 23.7%; Score 308.5; DB 22; Length 245;
XX Best Local Similarity 33.3%; Pred. No. 3.8e-21;
XX Matches 83; Conservative 38; Mismatches 109; Indels 19; Gaps 5;
XX
XX 15 TTGASGAGLTAERLVGOGASAVLLD-----LPNSGGEAOAKKGNVYFAPADVTSKD 70
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 10 TNGSTRIGICKAVLAFAKEGANIVLNGRSEITPEGRQIEEA--FEVKCIGISGDISDPA 67
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 71 VGTALALAKGKGRVDVAVNCAGIYVASTYVNLKGGQTHLEDPEFVLDVNLMTGFNVIR 130
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 68 AGEMIAQATVDQIGSIDILVNNNGIT-----NDKLLKRTKEDFNACLDINLVGFNMTQ 121
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 131 LVAGEGQNEPDGQGRGYIINTASYAAFEQVGAASASAGSAGIVGNTLPRIADLPATIG 190
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 122 QAVKRMKKO-----RSGRIINMAVSGLMGVGOANAAASAGVGGFTKSVAREVAPRG 175
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 191 IRMTAPGFGFGLTSLPEKVCNPLASQVFPFSLGDPAPAYAHVQAIIINPFLNGEV 250
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 176 ITGNALAPGFIQEMTDVLSKVKYIQMNOIPLQT-FQGVEDVVAATATLAKSPITIGV 234
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 251 IRLDGAIRM 259
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 235 VNVGGGLVM 243
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX
XX RESULT 21
XX ABB48892 standard; Protein; 247 AA.
XX
XX ABB48892;
XX
XX 05-FEB-2002 (first entry)
XX
XX DE Listeria monocytogenes protein #1596.
XX
XX XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
XX KM vitamin B12; bacterial infection; disease.
XX
XX OS Listeria monocytogenes.
XX
XX FN WO200177335-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF * 11-APR-2001; 2001WO-FR01118.

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XX
XX 11-APR-2000; 2000FR-0004629.
XX
XX (INSP ) INST PASTEUR.
XX
XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsalhi H, Dehoux P;
XX Dussurget O, Chehoudani F, Nedjati H, Glaser P, Kunst P,
XX Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA,
XX Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
XX Chakraborty T, Doman E, Hain T, Berche P, Charbit A, Durant L;
XX Perez-Diaz J, Baguerio F, Garcia Del Portillo F, Gomez-Lopez N;
XX Madueno E, De Pablo B, Wehland J, Kaerst U, Entian K, Hauf J;
XX Rose M, Voss H;
XX
XX MPI; 2002-010914/01.
XX
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX and prevention of Listeria and related bacterial infections, and
XX related polypeptides -
XX
XX Claim 6; SEQ ID No 1597; 192pp; French.
XX
XX The present invention relates to the genome sequence of Listeria
XX monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
XX it are useful for selecting probes and primers for detecting genes in L.
XX monocytogenes and related organisms, and for studying genetic
XX polymorphisms and other genomes. The present sequence is a protein
XX encoded by the genome sequence of the present invention. Proteins
XX expressed from the genome sequence are useful for raising specific
XX antibodies, identification of L. monocytogenes and related organisms, and
XX for biosynthesis and biodegradation, especially biosynthesis of Vitamin
XX B12. The genome sequence and proteins encoded by it are also useful for
XX selecting compounds that regulate gene expression and cell replication
XX and modulate L. monocytogenes-related diseases. In addition, the genome
XX sequence and proteins encoded by it are useful in pharmaceutical and
XX vaccines compositions for the treatment or prevention of infections by L.
XX monocytogenes and related organisms.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 247 AA;
XX
XX Query Match 23.7%; Score 308.5; DB 23; Length 247;
XX Best Local Similarity 32.3%; Pred. No. 3.8e-21;
XX Matches 86; Conservative 45; Mismatches 102; Indels 33; Gaps 7;
XX
XX 7 SVKGIYAVITGAGSLGIATTAERLVGOGASAVLLDLPNSGGEAOA---KKL---GNNV 58
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 2 TLGGVAVAVITGSGSIGRIDINILNAKEGANIFF---NNGSPPEAEETAKLVAHEGVEV 57
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 59 VFAPADVTSEKDVOPALALANGKFGKGRVDVAVNCAGIYVASTYVNLKGGQTHLEDPEFRLV 118
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 58 EAMKANVAIADVDVAFEFKQALIERGKVDILVNNNGITFRDNLMMRKE-----DEMDVI 111
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 119 DVNLMTGFNVIRLVAGEGQNEPDGQGRGYIINTASYAAFEQVGAASASAGSAGIVGM 178
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 112 NINLKGITFLCTKRAVSRIMKKO-----RAGKIINMAVSVGLIGNAGQANVYASRAGVIGL 165
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 179 TLPIARDLAPIGIRVMTAPGLFGTFLTSLPEKVCNPLASQVFPFSLGDPAPAYAHVQ 238
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 166 TKTARELAPRGINAVAVAPGFIITDMDKIDKEKTKEMLAQIP---LGAYGTTEDIAN 221
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 239 AII-----ENPFLNGEVIRLDGAIRM 259
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 222 AVLFLASDAKSIITIGQITLSVDGMYM 247
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX
XX RESULT 22
XX AAY95746
XX
XX ID AAY95746 standard; Protein; 247 AA.
XX
XX AC AAY95746;

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a Type II fatty acid synthetase. The enzyme has an extremely high

DR WFL; 2001-011455/10  
DR N-PSDB; AAS53187.





PR 17-JUN-2000; 2000US-0596193.  
 PR 14-JUN-2000; 2000US-0616847.  
 PR 19-SEP-2000; 2000US-0665363.  
 PR 20-OCT-2000; 2000US-0693267.  
 XX  
 PA (HXSE-) HXSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;  
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;  
 XX  
 DR WPI: 2001-589934/66.  
 DR N-PSDB; AAS45244.  
 XX  
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries  
 PT prepared from various human tissues, for diagnosis and treatment of  
 PT cancer, neurological, inflammatory, and autoimmune disorders -  
 XX  
 PS Example 2; SEQ ID No 701; 107pp; English.  
 XX  
 CC The invention relates to novel isolated human secreted polypeptides (I)  
 CC and polynucleotides (II). (I) and (II) are useful for treating  
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,  
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is  
 CC involved in increasing haematopoiesis, stem cell survival, bone growth  
 CC and remodeling. (I), (II) and modulators of (II) are useful for  
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for  
 CC creating transgenic animals useful for studying the in vivo activities of  
 CC the polypeptide as well as for studying modulators of the polypeptides.  
 CC (I) induces the proliferation of neural cells and regeneration of nerve  
 CC and brain tissue and is useful for the treatment of central and  
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,  
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral  
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis and is useful for treating myeloid  
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
 CC tissue growth, and in tissue repair, healing of burns, incisions,  
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative  
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for  
 CC gut protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues, various immune deficiencies and  
 CC disorders including severe combined immunodeficiency (SCID), bacterial or  
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,  
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic  
 CC reactions and conditions, such as asthma or other respiratory problems.  
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,  
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of  
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides  
 CC analgesic effects or other pain reducing effects, immunoglobulin like  
 CC activity and can act as an antigen in a vaccine composition to raise an  
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein  
 CC amino acid sequences of the invention.  
 XX  
 SO Sequence 257 AA:  
 Query Match 24.3%; Score 317; DB 22; Length 257;  
 Best Local Similarity 31.5%; Pred. No. 6.3e-22;  
 Matches 82; Conservative 42; Mismatches 110; Indels 26; Gaps 5;

DB 180 RALAEVARKLRVNVVAPGVHTMDTRDKBE--HLKKNIPL-GREGTEIYVAHAYVF 235  
 QY 240 ILENPLNGEYTRLDGAIRM 259  
 DB 236 LLESPITGSHVLYVDGIDL 255  
 RESULT 15  
 AAMS0255  
 ID AAMS0255 standard; Protein; 237 AA.  
 XX  
 AC AAMS0255;  
 XX  
 DT 21-JAN-2002 (first entry)  
 XX  
 DE Human dehydrogenase 21509.  
 XX  
 KW Dehydrogenase; human; ovarian cancer; colon cancer; lung cancer;  
 KW liver cancer; metastasis; antitumour; therapy; diagnosis.  
 OS Homo sapiens.  
 XX  
 FH Key  
 FH Domain  
 FT Location/Qualifiers  
 FT 3..229  
 FT /note="short-chain alcohol dehydrogenase domain"  
 FT 148..158  
 FT /note="short-chain alcohol dehydrogenase family  
 FT signature"  
 FT 114..116  
 FT /note="O-phosphorylated by protein kinase C"  
 FT 66..69  
 FT /note="O-phosphorylated by casein kinase II"  
 FT 95..98  
 FT /note="O-phosphorylated by casein kinase II"  
 FT 9..14  
 FT /note="N-myristoylated"  
 FT 38..43  
 FT /note="N-myristoylated"  
 FT 110..115  
 FT /note="N-myristoylated"  
 FT 128..133  
 FT /note="N-myristoylated"  
 FT 134..139  
 FT /note="N-myristoylated"  
 FT 153..158  
 FT /note="N-myristoylated"  
 FT  
 PN MO200175119-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 02-APR-2001; 2001WO-US10720.  
 XX  
 PR 31-MAR-2000; 2000US-193920P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Meyers RA, Rudolph-Owen LA;  
 XX  
 DR WPI: 2001-626438/72.  
 DR N-PSDB; AAI70573.  
 XX  
 PT Novel isolated 21509 and 33770 polypeptides belonging to human  
 PT dehydrogenase family members, useful for treating cancer, diabetes,  
 PT atherosclerosis, glomerulonephritis, Crohn's disease, cirrhosis,  
 PT multiple sclerosis -  
 XX  
 PS Claim 1(a); Fig 2; 146pp; English.  
 XX  
 CC The present sequence is that of a novel human dehydrogenase,  
 CC designated 21509. The protein has a significant number of  
 CC structural characteristics in common with members of the  
 CC dehydrogenase/oxidoreductase family. Its expression pattern

CC acids are useful for detecting the presence of proteins essential for the  
 CC viability of a bacterial cell wall in samples such as cells, tissues,  
 CC biological fluids, blood, serum, nose, ear or throat swabs with ligands,  
 CC and for detecting corresponding target nucleic acid molecules with  
 CC complementary sequences. The nucleic acids are also useful for  
 CC determining whether a genomic nucleotide sequence of interest is  
 CC essential for viability of a bacterial cell or whether it resides within  
 CC an operon, by integrating an exogenous nucleotide sequence comprising a  
 CC portion of an open reading frame of the genomic sequence of interest  
 CC (comprising 200-500 base pairs) into the genomic sequence of interest  
 CC which confers a selectable phenotype to the cell, and determining cell  
 CC viability with a selection agent such as chloramphenicol. The nucleic  
 CC acids and proteins are also useful as vaccines and for treating bacterial  
 CC infections with gene therapy and antisense therapy. The nucleic acids  
 CC also enable identification of targets suitable for the treatment of  
 CC antibiotic resistant bacterial infections.

XX Sequence 243 AA:

Query Match 25.3%; Score 330.5; DB 22; Length 243;  
 Best Local Similarity 35.1%; Pred. No. 3.1e-23;  
 Matches 88; Conservative 37; Mismatches 103; Indels 23; Gaps 6;

QY 15 TGGAGAGLATAERLVGAGASAVLLDLPNSGGE-----AQAKKLGNNVYFAPADVISE 68  
 DB 10 TGGAGAGLATAERLVGAGASAVLLDLPNSGGE-----AQAKKLGNNVYFAPADVISE 65  
 QY 69 KDVQALALAKGFEGRVDVAVNCAGIAVASKTYNLRKGGTHTLEDFORYLVNMGTRV 128  
 DB 66 AAKRMIDDAIEELGSDVAVLNAGI--TQDTLMK-----TEAEFEKLVKNLNGARNM 119  
 QY 129 IRLVAGEMGNEPDGQGRGVITNTASVAFEGOVQOAYASAKSGIYGMTPIARDLAP 188  
 DB 120 TQGVV-----KPMARREGAIIIMSSVYGLMGNIGQANYASAKGLIGFTSVAREVAS 173  
 QY 189 IGRVNTAPGLFGTPLTSLPEKYCNFLASQVPEPSRLGDPAEVAHLVQAIITENPFLNG 246  
 DB 174 RTRVNVVIAAPGMIESDMTALILSDRIKATLQIPM-KFEGQAEQVADTLVFLAGODYLNG 232  
 QY 249 EVIRLDGAIEM 259  
 DB 233 QVVAIDGGLSM 243

# RESULT 13

ABBS4087 ID ABB54087 standard; Protein; 243 AA.

AC ABB54087;

DT 16-MAY-2002 (first entry)

DE Lactococcus lactis protein dabG1.

KW Biosynthesis: biodegradation; lactic bacterium; yogurt; cheese.

OS Lactococcus lactis IL1403.

PN FR2807446-A1.

PD 12-OCT-2001.

PF 11-APR-2000; 2000FR-0004630.

PR 11-APR-2000; 2000FR-0004630.

PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.

PI Boletine A, Sorokline A, Renault P, Ehrlich SD;

DR WPI; 2002-043418/06.

PT New nucleotide sequence useful in the identification or Lactococcus

PT Lactis and related species -  
 XX Claim 6; SEQ ID No 789; 2504pp; French.

XX The present invention is related to a Lactococcus lactis nucleotide  
 CC sequence (AA028344) and related proteins (ABBS3300-ABBS5621). The  
 CC nucleic acid sequence is useful in the detection and/or amplification of  
 CC related species. The proteins of the invention are useful for the  
 CC biosynthesis or biodegradation of a composition of interest. The  
 CC invention helps research in lactic bacteria, particularly useful in the  
 CC production of yogurt and cheese.  
 CC Note: The sequence data for this patent is based on equivalent patent  
 CC WO2001/77334 (published 18-OCT-2001) which is available in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 243 AA:

Query Match 24.9%; Score 324.5; DB 23; Length 243;  
 Best Local Similarity 31.7%; Pred. No. 1.1e-22;  
 Matches 82; Conservative 48; Mismatches 104; Indels 25; Gaps 6;

QY 8 VKGLVAVITGASGLGATAERLVGAGASAVLLDLPNSGGEAOKL-----GNVYF 60  
 DB 3 IKNNVFEVGTGTRIGKALALQFAKASNLII-----NGSALSEELAEFTAYGAVAG 57  
 QY 61 APADVSEKDVQALALAKGFEGRVDVAVNCAGIAVASKTYNLRKGGTHTLEDFORYLV 120  
 DB 58 ISGDISKEDKQAVAEIETLGSVDILVNNAGI--TRDGLSKMSE-----EDPEVYK 111  
 QY 121 NLMGTENVIRLVAGEMGNEPDGQGRGVITNTASVAFEGOVQOAYASAKSGIYGMTL 180  
 DB 112 NLTGAFNMTQAVL-----KPMTRARSGAIIIMSSVYGLMGNIGQANYASAKGLIGFT 165  
 QY 181 PIARDIATIGRVNTAPGLFGTPLTSLPEKYCNFLASQVPEPSRLGDPAEVAHLVQAI 240  
 DB 166 SIARVAAARNVAVNAPGLIESDMTEVLSKVADAMKGOIPM-KRGMPEIATATQFL 224  
 QY 241 IENPFLNGEVRLDGAIEM 259  
 DB 225 AEQEVMTGQVLTIDGVSIM 243

# RESULT 14

AAU28344 ID AAU28344 standard; Protein; 257 AA.

AC AAU28344;

DT 18-DEC-2001 (first entry)

DE Novel human secretory protein, Seq ID No 701.

KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;  
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
 KW amyotrophic lateral sclerosis; platelet disorder; peridontal disease;  
 KW ulcer; osteoporosis; bone degenerative disorder; infectious disease;  
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
 KW fertility; analgesic; pain; antigen.

OS Homo sapiens.

PN WO200166689-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US04942.

PR 07-MAR-2000; 2000US-0519705.  
 19-MAY-2000; 2000US-0574454.



Db 66 ADARKMIDQAIKELGSDVLYNNAGI--TQDTMLKMK---TEADFEKYLKVNLTGAFNM 119  
 QY 129 IRLVAGEMGNEDPDGGRGVITINTASYAAFEQVQGAAYSAKSGIYGMTLPIDRLAP 188  
 Db 120 TQSVL-----KPMKARREGALINMSVGLMGNIGQANVYASKAGLIGFTKSVAREVAS 173  
 QY 189 IGIRVNTIAPGLFGTLPILTSLEPKVCNPLASQVPPPSRLGDPAEYAHLYQALIENTPFLNG 248  
 Db 174 RNIRVNVIAFGMIESDMETALISDKIKETLAQIPM-KEFGQAEQVADLTVPFLAGQDYLTG 232  
 QY 249 EVIRLDGAIKM 259  
 Db 233 QVTAIDGGLSM 243

## RESULT 11

AAU37988

ID AAU37988 standard; Protein: 243 AA.

AC AAU37988;

DT 14-FEB-2002 (first entry)

DE Streptococcus pneumoniae cellular proliferation protein #417.

KM Antisense; prokaryotic cellular proliferation protein;

KW antibiotic; antibacterial; drug design.

OS Streptococcus pneumoniae.

PN W0200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

DR WPI; 2001-611495/70.

DR N-PSDB; AAS55847.

XX New polynucleotides for the identification and development of

XX antibiotics, comprise sequences of antisense nucleic acids -

XX Example 3; Seq ID No 13581; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to

XX prokaryotic cellular proliferation, their use in identifying the

XX genes, their use in the discovery of novel antibiotics, the essential

XX genes themselves and the encoded proteins. The prokaryotes used are

XX *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*

XX *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The

XX invention is also useful for the identification of potential new targets

XX for antibiotic development. The antisense nucleic acids can also be used

XX to identify proteins used in proliferation, to express these proteins,

XX and to obtain antibodies capable of binding to the expressed proteins.

XX The proteins can be used to screen compounds in rational drug discovery

XX programmes. The antisense nucleic acid sequence is also useful to screen

XX for homologous nucleic acids which are required for cell proliferation in

XX a wide variety of organisms. The present sequence represents an

XX essential prokaryotic cellular proliferation protein.

XX Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp://ipo.int/pub/published\_pct\_sequences.  
 XX

SO Sequence 243 AA;

Query Match 25.4%; Score 331.5; DB 22; Length 243;

Best Local Similarity 35.5%; Pred. No. 2,5e-23;

Matches 89; Conservative 36; Mismatches 103; Indels 23; Gaps 6;

QY 15 ITGASGIGLATAEELVYGASAVLIDLPNNGE-----AQAKKLGNNVVFAPADVTSE 68  
 Db 10 ITGSSRGIGLATAEELVYGASAVLIDLPNNGE-----NSGATSEELAEFSYGIKVPISGDVDF 65  
 QY 69 KDVTALALAKGKRGVAVAVACAGIYASKTYNLKQOTHTLDFQKRVLYVNLMTFTNV 128  
 Db 66 ADARKMIDQAIKELGSDVLYNNAGI--TQDTMLKMK---TEADFEKYLKVNLTGAFNM 119  
 QY 129 IRLVAGEMGNEDPDGGRGVITINTASYAAFEQVQGAAYSAKSGIYGMTLPIDRLAP 188  
 Db 120 TQSVL-----KPMKARREGALINMSVGLMGNIGQANVYASKAGLIGFTKSVAREVAS 173  
 QY 189 IGIRVNTIAPGLFGTLPILTSLEPKVCNPLASQVPPPSRLGDPAEYAHLYQALIENTPFLNG 248  
 Db 174 RNIRVNVIAFGMIESDMETALISDKIKETLAQIPM-KEFGQAEQVADLTVPFLAGQDYLTG 232  
 QY 249 EVIRLDGAIKM 259  
 Db 233 QVTAIDGGLSM 243

## RESULT 12

AAU01032

ID AAU01032 standard; Protein: 243 AA.

AC AAU01032;

DT 02-OCT-2001 (first entry)

DE CFE 35 protein sequence.

KM Antibacterial; vaccine; gene therapy; bacterial cell wall viability;

KW CFE; CEG; Conserved Essential Gene; bacterial infection;

KW antisense therapy; antibiotic resistance.

OS Streptococcus pneumoniae.

PN W0200149721-A2.

PD 12-JUL-2001.

PF 29-DEC-2000; 2000WO-US35604.

PF 30-DEC-1999; 99US-0174089.

PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

PI Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Brucoleri RE;

PI Thannassi JA;

DR WPI; 2001-496721/54.

DR N-PSDB; AAH90731.

XX Nucleic acids encoding conserved essential genes involved in bacterial

XX replication which are potential targets for the treatment of antibiotic

XX resistant bacterial infections -

XX Claim 27; Page 273; 380pp; English.

XX The present invention relates to nucleic acids (AAH90701-AAH90918)

XX encoding polypeptides (AAU01002-AAU01114), which are essential for the

XX viability of a bacterial cell wall. The acronym CFE stands for "CEG For

XX Expression", where CEG stands for "Conserved Essential Gene". The nucleic

[illegible][illegible]



Query Match 51.0%; Score 664.5; DB 18; Length 388;  
 Best Local Similarity 55.5%; Pred. No. 1.1e-54;  
 Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLAVITGGASGLTAEELVGGASAVLLDLPNSGSAOKKLGNNVFAADYTS 67  
 DB 143 IEGRFVVTGAAASGSAKLAOGKAVYLADI-----AEKDAPEGVHAACDVTD 196  
 QY 68 EKDVPALALAKGKRGVAVNCAGIAVASKTYNLKKGQTHLEDFQRLVDVLMGTFN 127  
 DB 197 ATAAQTALATDRGRDLGVCAGIAPARM--LGRDGHGIDSEFAAVTINLIGSFN 254  
 QY 128 VRLVAGSEMGONEPPOGGORGVIIINTASVAFEGVGQAASAKGIVGWTLEIARDLA 187  
 DB 255 MARLAEAMARNEYR-GERGVYNTASTIAADGQIGVATASAGVATLPAARDLA 313  
 QY 188 PIGIRVMTIAPGLFGTPLLTSLEPKVCNFIASQVFPFSLDPAEYAHVQAIIENPFLN 247  
 DB 314 RGIKRVMTIAPGIFRTPLMEGLPDQVODSLGAAYVFPRLCEPSEYALLHIIIANPMLN 373  
 QY 248 GEVIRLDGAIRMQ 261  
 DB 374 GEVIRLDGALRMAP 387

RESULT 6  
 ABP28011  
 ID ABP28011 standard; Protein; 244 AA.

XX ABP28011;  
 DT 02-JUL-2002 (first entry)  
 XX Streptococcus polypeptide SEQ ID NO 5198.  
 DE Streptococcus polypeptide SEQ ID NO 5198.  
 XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
 XX antiinflammatory; infection; vaccine; meningitis; gene therapy.  
 OS Streptococcus agalactiae.  
 XX MO200234771-A2.  
 PN 02-MAY-2002;  
 PD 29-OCT-2001; 2001WO-GB04789.  
 XX 27-OCT-2000; 2000GB-0026333.  
 PR 24-NOV-2000; 2000GB-0028727.  
 PR 07-MAR-2001; 2001GB-0005640.  
 XX (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;  
 PI Tettelin H;  
 DR WPI: 2002-352536/38.  
 DR N-PSDB: ABN68642.  
 XX New Streptococcus protein for the treatment or prevention of infection  
 PT or disease caused by Streptococcus bacteria, such as meningitis, and  
 PT for detecting a compound that binds to the protein -  
 XX Claim 1; Page 3663; 4525pp; English.  
 PS The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins.

Sequence 244 AA;  
 S0

Query Match 28.1%; Score 366.5; DB 23; Length 244;  
 Best Local Similarity 36.9%; Pred. No. 1.2e-26;  
 Matches 93; Conservative 38; Mismatches 98; Indels 23; Gaps 5;

QY 15 ITGASGLGATAEELVGGASAVLLDLPNSGGE-----AQAKKLGNNVFAADYTS 68  
 DB 10 ITGSSRGIGLAIHQFQGLANIVL-----NGRSEISDLAEADYGVKIALSGVSS 65  
 QY 69 KDVPALALAKGKRGVAVNCAGIAVASKTYNLKKGQTHLEDFQRLVDVLMGTFN 128  
 DB 66 EDANRMKIKFAIASLGSVDVLYNNAGIT-----NDKIMLMTVEDEFSYKINLTGAFNM 119  
 QY 129 IRLVAGSEMGONEPPOGGORGVIIINTASVAFEGVGQAASAKGIVGWTLEIARDLA 188  
 DB 120 TQSVL-----KPKTRKRGAIINISSVGLTGVGQANAAASKAGLIGTRKVAAREVA 173  
 QY 189 IGIKRVMTIAPGLFGTPLLTSLEPKVCNFIASQVFPFSLDPAEYAHVQAIIENPFLN 248  
 DB 174 RGIKRVMTIAPGLFISDVTDIPEKMQAIIAQIPM-KRICKGKVAQVAFLEAOEYLTG 232  
 QY 249 EVIRLDGAIRMQ 260  
 DB 233 QVIRLDGQMTWQ 244

RESULT 7  
 ABP27345  
 ID ABP27345 standard; Protein; 243 AA.

XX ABP27345;  
 AC 02-JUL-2002 (first entry)  
 DT Streptococcus polypeptide SEQ ID NO 3866.  
 DE Streptococcus polypeptide SEQ ID NO 3866.  
 XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
 XX antiinflammatory; infection; vaccine; meningitis; gene therapy.  
 OS Streptococcus pyogenes.  
 XX MO200234771-A2.  
 PN 02-MAY-2002;  
 PD 29-OCT-2001; 2001WO-GB04789.  
 XX 27-OCT-2000; 2000GB-0026333.  
 PR 24-NOV-2000; 2000GB-0028727.  
 PR 07-MAR-2001; 2001GB-0005640.  
 XX (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;  
 PI Tettelin H;  
 DR WPI: 2002-352536/38.  
 DR N-PSDB: ABN67976.



Query Match	87.1%	Score 1136	DB 20	Length 227
Best Local Similarity	99.6%	Pred. No. 8.9e-100		
Matches 226	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Sequence 227 AA:				
35 ASAVLLDLPNSGGEAOAKRLGNVVPAPADVTSEKDVOTALALAKGRGVDVAVNCAGI	94			
1 ASAVLLDLPNSGGEAOAKRLGNVVPAPADVTSEKDVOTALALAKGRGVDVAVNCAGI	60			
95 AVASKTYNLKKGGTHLEDFQRYLVQVNLMLGTFNNVIRLVAAGMGQNEPDGGGRVITNTA	154			
61 AVASKTYNLKKGGTHLEDFQRYLVQVNLMLGTFNNVIRLVAAGMGQNEPDGGGRVITNTA	120			
155 SVAAFEQGVQQAAYSAKSGGIYGMPLPIARDLAPIGIVMTIAPQLRGTPLLSPEKVC	214			
121 SVAAFEQGVQQAAYSAKSGGIYGMPLPIARDLAPIGIVMTIAPQLRGTPLLSPEKVC	180			
215 NFPLASQVPPFSRLGDDPAEYAHYVQALITENPFLANGEVIRLDDAIRNQP	261			
181 NFPLASQVPPFSRLGDDPAEYAHYVQALITENPFLANGEVIRLDDAIRNQP	227			
RESULT 3				
ID AAY32239 standard; Protein; 260 AA.				
AC AAY32239;				
XX 15-FEB-2000 (first entry)				
XX Alzheimer-associated beta-amyloid binding protein (ERAB).				

XX		Alzheimer-associated beta-amyloid binding protein; ERAB; mouse;
KM	Leydig cell; differential display RT-PCR; DDRT-PCR;	
KM	Short chain alcohol dehydrogenase; SCAD; testis marker;	
KM	Spermatogenesis.	
XX		
OS	Mus musculus.	
FH		
FH	Key	Location/Qualifiers
FT	Region	10..15
FT	Region	/note= "beta sheet region A"
FT	Region	18..32
FT	Region	/note= "alpha helix region A"
FT	Region	35..41
FT	Region	/note= "beta sheet region B"
FT	Region	43..57
FT	Region	/note= "alpha helix region B"
FT	Region	61..66
FT	Region	/note= "beta sheet region C"
FT	Region	70..80
FT	Region	/note= "alpha helix region C"
FT	Region	84..94
FT	Region	/note= "beta sheet region D"
FT	Region	109..133
FT	Region	/note= "alpha helix region D"
FT	Region	143..153
FT	Region	/note= "beta sheet region E"
FT	Region	167..171
FT	Region	/note= "SCAD motif"
FT	Region	185..186
FT	Region	/note= "alpha helix region A"
FT	Region	190..196
FT	Region	/note= "beta sheet region F"
FT	Region	204..218
FT	Region	/note= "alpha helix region F"
FT	Region	247..252
FT	Region	/note= "beta sheet region G"
XX		
PN	WO9594347-A2.	
XX		
PD	28-OCT-1999.	
XX		
PE	19-APR-1999; 99WO-EP02610.	
XX	17-APR-1998; 98US-0082257.	
PR	(HORM-) INST HORMON & FORPFLANZUNGSFORSCHUNG GM.	
FA	Ivell R, Spiess A, Balvers M, Jaehner D, Hansis C;	
PI	WPI; 2000-052699/04.	
XX	N-PESDB; AA234663.	
DR		
XX	Noval differential display reverse transcription PCR method used to	
PT	detect genes expressed in mutant tissues -	
PS	Claim 4; Fig 2; 40pp; English.	
XX		
CC	This sequence represents murine Alzheimer-associated beta-amyloid	
CC	binding protein (ERAB, see AY132239), a novel member of the SCAD	
CC	(short chain alcohol dehydrogenase) family of steroid metabolising	
CC	and related enzymes. The sequence was deduced from cDNA (see	
CC	AA234663). Identified using a novel differential display RT-PCR method	
CC	for analysis of w/wv mouse testis gene products. ERAB is	
CC	specifically upregulated in the testicular Leydig cells of w/wv	
CC	azoospermic mutant mice, suggesting an important role in the	
CC	establishment and support of spermatogenesis. The invention also	
CC	relates to vectors, host cells, methods for expressing the ERAB	
CC	nucleic acid, and antibodies. The nucleic acid and protein are	
CC	useful e.g. as markers for testicular development.	
XX		
XX	Sequence 260 AA;	

84 266 20.4 285 22 AAV34648 E. coli cellular p  
85 264.5 20.3 246 22 AAE02195 S. aureus NADPH-de  
86 263 20.2 243 23 AAB54107 Lactococcus lactis  
87 263 20.2 261 13 AAR27756 NAD affinity gluc  
88 263 20.2 276 21 AAY54416 Secoisolaricresin  
89 263 20.2 276 23 AAO21494 Secoisolaricresin  
90 262.5 20.1 286 22 AAV36267 Pseudomonas aerugi  
91 261 20.0 272 21 AAB10740 B. megaterium gluc  
92 261 20.0 340 21 AAY54413 H. ghilani1/3. me  
93 260 19.9 277 21 AAY54413 Secoisolaricresin  
94 258.5 19.9 273 21 AAY54413 Secoisolaricresin  
95 259 19.9 253 22 AAV36249 Pseudomonas aerugi  
96 257.5 19.7 243 23 ABB47402 Listeria monocytog  
97 257 19.7 247 16 AAR66291 Mycobacterium bovi  
98 257 19.7 247 16 AAR63899 M. bovis p85 ORF1  
99 257 19.7 247 18 AAM40809 M. bovis p85 opero  
100 257 19.7 261 23 AAE20115 Lactobacillus rham

## ALIGNMENTS

## RESULT 1

AAW71471 standard; Protein: 261 AA.

AAW71471;

16-DEC-1998 (first entry)

ERAB protein.

Endoplasmic reticulum associated amyloid-beta peptide binding protein;

ERAB protein; amyloid-beta peptide; inhibitor; demyelinating disease;

neurodegenerative disorder; therapy; Alzheimer's disease; schizophrenia;

Down's syndrome; Parkinson's disease; Huntington's disease;

multiple sclerosis.

Homo sapiens.

WO9840484-A1.

17-SEP-1998.

12-MAR-1998; 98WO-US04915.

12-MAR-1997; 97US-0815225.

(UYCO) UNIV COLUMBIA NEW YORK.

Stern DM, Yan SD;

WPI; 1998-531524/45.

N-PSDB; AAV60576.

Endoplasmic reticulum associated amyloid-beta peptide binding

Protein - Inhibitors of which can be used to treat neurodegenerative

disorders

Claim 2; Fig 1D; 53pp; English.

This sequence is the endoplasmic reticulum associated amyloid-beta peptide binding (ERAB) protein of the invention. The protein can be used in a method for evaluating the ability of an agent to inhibit binding of ERAB polypeptide to amyloid-beta peptide comprising: (a) incubating the ERAB polypeptide, the agent and amyloid-beta peptide under binding conditions; (b) determining the amount of amyloid-beta peptide bound to ERAB polypeptide; (c) comparison of the amount of binding with results from a control using no agent, so determining inhibition ability of the agent. The inhibitors identified by the method can be used to treat a neurodegenerative condition by administration of an agent that inhibits binding of an ERAB polypeptide to amyloid-beta peptide, particularly where the disease is Alzheimer's disease, Down's syndrome, Parkinson's

CC disease, Huntington's disease, schizophrenia, a demyelinating disease, or  
CC multiple sclerosis. The inhibitors can also be used to treat other  
CC neurodegenerative conditions including those associated with ageing,  
CC dentatorubral and pallidolysian atrophy, Machado-Joseph disease,  
CC muscular dystrophy, senility, spinocerebellar ataxia type I, spinobulbar  
CC muscular atrophy, stroke, and trauma.

SQ Sequence 261 AA;

Query Match 99.6%; Score 1299; DB 19; Length 261;

Best Local Similarity 99.6%; Pred. No. 3.5e-115;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSVKGVLAVITGGASGGLATAEKLVGQGSASVLLDPNSGGGAQAKLNNVVF 60

DB 1 MAACRSVKGVLAVITGGASGGLATAEKLVGQGSASVLLDPNSGGGAQAKLNNVVF 60

QY 61 APADVTSEKDVOTATLAKKFGKRVDAVNCAGIAVASTYMLKKQHTLLEDFORVLDV 120

DB 61 APADVTSEKDVOTATLAKKFGKRVDAVNCAGIAVASTYMLKKQHTLLEDFORVLDV 120

QY 121 NLMGTFNVIRLVAGENGQNEPDGGGGRGVYINTASVAAREGGVGAAYASASGIGYKTL 180

DB 121 NLMGTFNVIRLVAGENGQNEPDGGGGRGVYINTASVAAREGGVGAAYASASGIGYKTL 180

QY 181 PIARDLAPIGIRMTIAPGLFETPLTSLPEKYNFLASGVPPPSRLGPAEYAHLYQAI 240

DB 181 PIARDLAPIGIRMTIAPGLFETPLTSLPEKYNFLASGVPPPSRLGPAEYAHLYQAI 240

QY 241 IENPFLNGEVIRLDGAIRMOP 261

DB 241 IENPFLNGEVIRLDGAIRMOP 261

RESULT 2

AAW67934 standard; Protein: 227 AA.

AAW67934;

25-MAR-1999 (first entry)

Fragment of human secreted protein encoded by gene 8.

Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;

developmental abnormality; foetal deficiency; blood; allergy; renal;

immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;

inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;

cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

WO9842738-A1.

01-OCT-1998.

19-MAR-1998; 98WO-US05311.

30-MAY-1997; 97US-0050937.

21-MAR-1997; 97US-0041276.

21-MAR-1997; 97US-0041277.



Thu Jun 26 06:55:09 2003

us-09-931-186-6.rag

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OW protein - protein search, using sw model

Run on: June 23, 2003, 14:19:21 ; Search time 39.6667 Seconds

(without alignments)  
876.767 Million cell updates/sec

Title: us-09-931-186-6

Perfect score: 1304  
Sequence: 1 MAACRSVKGLIVATGGAS.....ENPFLNGEVRRLDGAIRMP 261

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

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22: /SID2/gcgdata/geneseq/geneeqp-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneseq/geneeqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1399	99.6	261	19	AAW71471
2	1136	87.1	227	21	AAW67934
3	1134	87.0	260	21	AAI32239
4	913	70.0	255	18	ABW62988
5	664.5	51.0	388	22	AAW65513
6	366.5	28.1	244	23	ABP28011
7	356	27.3	243	23	ABP27345
8	331.5	25.4	243	19	AAW60670
9	331.5	25.4	243	21	AAW5706
10	331.5	25.4	243	22	AAU37767

11	331.5	25.4	243	22	AAU37988	Streptococcus pneu
12	330.5	25.3	243	22	AAW01032	CFE 35 protein seq
13	324.5	24.9	243	23	ABW54087	Lactococcus lactis
14	317	24.3	257	22	AAU28344	Novel human secret
15	314	24.1	237	22	AAW50255	Human dehydrogenas
16	312.5	24.0	241	22	AAW96397	Putative P. abyssal
17	312	23.9	237	22	AAU28156	Novel human secret
18	312	23.9	237	22	AAU19928	Human oxidoreducta
19	310.5	23.8	248	21	AAV54422	Amino acid sequenc
20	308.5	23.7	245	22	AAU35328	Enterococcus faeca
21	308.5	23.7	247	23	ABW48692	Listeria monocyctog
22	301	23.1	247	21	AAV95746	Bacillus megaterium
23	297.5	22.6	267	22	AAW47459	Levodione reductas
24	295	22.6	263	23	ABP39667	Staphylococcus epi
25	294	22.5	262	22	AAW83032	S. epidermidis ope
26	292.5	22.4	303	23	ABW63537	G. suboxydans DSM
27	292.5	22.4	303	23	ABW92624	Herbicideallly activ
28	291	22.3	315	17	AAW89323	Rape leaf beta-ket
29	291	22.3	315	17	AAW89322	Rape seed beta-ket
30	290.5	22.3	270	20	AAU41761	Human PRO474 prote
31	290.5	22.3	270	21	AAW44317	Human PRO474 prote
32	290.5	22.3	270	21	AAW44317	Human PRO474 prote
33	290.5	22.3	270	22	AAU28108	Novel human secret
34	290.5	22.3	279	22	AAU18296	Human endocrine po
35	290.5	22.3	288	22	AAU28296	Novel human secret
36	289.5	22.2	244	21	AAV54421	Amino acid sequenc
37	289.5	22.2	244	22	AAU34533	E. coli cellular p
38	289.5	22.2	246	12	AAU10974	Acetoacetyl CoA re
39	288.5	22.1	246	10	AAW94157	Acetyl-CoA reducta
40	288.5	22.1	246	14	AAW32192	Sequence encoded b
41	288.5	22.1	246	20	AAW43310	Acetoacetyl-CoA re
42	288.5	22.1	246	21	AAV54423	Amino acid sequenc
43	288.5	22.1	246	22	AAW71981	Rastonia aetutropha
44	288.5	22.1	282	21	AAW44578	Xytilol dehydrogen
45	288.5	22.1	339	16	AAW71324	Acetyl-CoA-reducta
46	286.5	22.0	270	21	AAW42558	Human ORF ORF222
47	285.5	21.9	254	22	AAW49773	Protein with acetyl
48	285.5	21.9	277	21	AAW54415	Secoisolactichresin
49	283.5	21.7	242	22	AAW59290	Protonlactiferium
50	282.5	21.7	253	23	ABW54214	Lactococcus lactis
51	282.5	21.6	283	10	AAW94155	Acetyl-CoA reducta
52	282	21.6	280	23	ABW92449	Herbicideallly activ
53	280.5	21.5	306	22	AAW81644	S. epidermidis ope
54	279.5	21.4	241	12	AAU10679	Acetoacetyl CoA re
55	279.5	21.4	246	14	AAW4761	Acetoacetyl CoA re
56	278.5	21.4	244	23	ABW39586	Staphylococcus epi
57	278	21.3	263	22	AAW38499	Salmonella typhi c
58	277	21.2	244	22	AAW81318	Human AFP protein
59	276.5	21.2	254	22	AAW47522	(R)-2-octanol dehy
60	276	21.2	258	22	AAW92682	C glutamicum prote
61	276	21.2	258	22	AAW79361	Corynebacterium gl
62	274.5	21.1	269	23	ABW92448	Herbicideallly activ
63	274	21.0	206	20	AAW9345	Short-chain dehyd
64	273.5	21.0	248	23	AAW36959	Chlamydia trachoma
65	273	20.9	186	19	AAW8474	S. pneumoniae 3-ox
66	273	20.9	202	23	AAU77210	Consensus protein
67	272.5	20.9	249	23	ABW39980	Staphylococcus epi
68	272.5	20.9	272	22	AAU37095	Staphylococcus aur
69	272.5	20.9	336	16	AAW06488	Malee T52 sequence
70	271.5	20.8	251	22	AAU34193	Staphylococcus aur
71	269	20.6	231	23	ABW39552	Staphylococcus epi
72	268.5	20.6	246	21	AAW15707	Staphylococcus aur
73	268.5	20.6	246	22	AAU33965	Staphylococcus aur
74	268.5	20.6	246	22	AAU36530	Staphylococcus aur
75	268.5	20.6	246	22	AAU37210	Staphylococcus aur
76	268.5	20.6	246	22	AAU37507	Staphylococcus aur
77	267	20.5	254	23	ABW48207	Listeria monocyctog
78	266.5	20.4	242	23	AAW5381	Haemophilus influe
79	266.5	20.4	262	23	AAU16940	Recombinant enzyme
80	266.5	20.4	252	23	AAV92509	Human OXR6-6. Hom
81	266.5	20.4	267	21	ABW5505	Arbidopsis thaila
82	266.5	20.4	268	22	ABW52552	Escherichia coli p
83	266.5	20.4	308	21	AAW35504	Arbidopsis thaila

Thu Jun 26 06:55:09 2003

Search completed: June 23, 2003, 14:35:41  
Job time : 14.1667 secs

us-09-931-186-6.ra1

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Thu Jun 26 06:55:09 2003

us-09-931-186-6.ra1

Page 11

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; TYPE: PR
; ORGANISM: Staphylococcus aureus
US-09-572-810A-2
Db 65 KSNIDMKLVDFHFGHIDIVNSAGOSLSKTTD-----YVEQDMIDWNIGTTH 118
QY 128 VIRLVAGEMGQNEPDGQGGGVYIINTASVAAFEGOVQAASAKGIVGMLPIARDLA 187
; 119 VLQATLPYLLKQ-----SSGHIIINLASVGFETPTNNAVYGAATKAIHAIQTSLKELA 172
QY 188 PIGIRVMTIAPGLFETPLTSLPEKVCNFIASQVFPFSRLGDPAEVAHLVQAIIEN--PF 245
; 173 RTGVKATVISPBMVDTPM 190
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RESULT 23
US-09-238-481-2
; Sequence 2, Application US/09238481
; Patent No. 6110704
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Fabg
; FILE REFERENCE: GMI0192
; CURRENT APPLICATION NUMBER: US/09/238,481
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 246
; TYPE: PR
; ORGANISM: Staphylococcus aureus
US-09-238-481-2
Query Match 20.6%; Score 268.5; DB 3; Length 246;
Best Local Similarity 28.7%; Pred. No. 6.8e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;
QY 13 AVITGASGLGLATAEERLVGQASAVLLDLPNSGGEQAQ-----KRLGNVVFAPADYTS 67
; 7 ALVTGASRGIGRSIALQIAEEGYN--VAANYAGSKKEAEVVEETKAGVDSFAIQANVAD 65
QY 68 EKDVOTATLALAKGKRGVADVAVNAGIAVASKTYNLKKQTHLEDFQRYLDVNLGTFN 127
; 66 ADEVKAMIKYVVSQSGSLDVLVNNAGITRDNLKMRKE-----QEMDVIDTFLKGVFN 119
Db 128 VIRLVAGEMGQNEPDGQGGGVYIINTASVAAFEGOVQAASAKGIVGMLPIARDLA 187
; 120 CIQKATPQMLRQ-----RSGAIIINLSVYGAAGVNPQANVATKAGVIGLTKSARELA 173
QY 188 PIGIRVMTIAPGLFETPLTSLPEKVCNFIASQVFPFSRLGDPAEVAHLVQAIIEN--PF 245
; 174 SRGITVNAVAPGFIVSDMTDALSDLEKQMLTQIPL--ARFGDDIDIANVAFIASDKAKY 232
QY 246 LNGEVIRLDGAIRM 259
; 233 ITGQTIHVNGMYM 246
Db 233 ITGQTIHVNGMYM 246
;
RESULT 24
US-09-572-810A-2
; Sequence 2, Application US/09572810A
; Patent No. 6365387
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Fabg
; FILE REFERENCE: GMI0192
; CURRENT APPLICATION NUMBER: US/09/572,810A
; CURRENT FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 09/238,481
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 246
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; TYPE: PR
; ORGANISM: Staphylococcus aureus
US-09-572-810A-2
Query Match 20.6%; Score 268.5; DB 4; Length 246;
Best Local Similarity 28.7%; Pred. No. 6.8e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;
QY 13 AVITGASGLGLATAEERLVGQASAVLLDLPNSGGEQAQ-----KRLGNVVFAPADYTS 67
; 7 ALVTGASRGIGRSIALQIAEEGYN--VAANYAGSKKEAEVVEETKAGVDSFAIQANVAD 65
QY 68 EKDVOTATLALAKGKRGVADVAVNAGIAVASKTYNLKKQTHLEDFQRYLDVNLGTFN 127
; 66 ADEVKAMIKYVVSQSGSLDVLVNNAGITRDNLKMRKE-----QEMDVIDTFLKGVFN 119
Db 128 VIRLVAGEMGQNEPDGQGGGVYIINTASVAAFEGOVQAASAKGIVGMLPIARDLA 187
; 120 CIQKATPQMLRQ-----RSGAIIINLSVYGAAGVNPQANVATKAGVIGLTKSARELA 173
QY 188 PIGIRVMTIAPGLFETPLTSLPEKVCNFIASQVFPFSRLGDPAEVAHLVQAIIEN--PF 245
; 174 SRGITVNAVAPGFIVSDMTDALSDLEKQMLTQIPL--ARFGDDIDIANVAFIASDKAKY 232
QY 246 LNGEVIRLDGAIRM 259
; 233 ITGQTIHVNGMYM 246
Db 233 ITGQTIHVNGMYM 246
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RESULT 25
US-09-504-358-14
; Sequence 14, Application US/09504358
; Patent No. 6365376
; GENERAL INFORMATION:
; APPLICANT: Brostowicz, Patricia C.
; APPLICANT: Rouviere, Pierre E.
; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIIC ACID INTERMEDIA
; FILE REFERENCE: BC1001 US NA
; CURRENT APPLICATION NUMBER: US/09/504,358
; CURRENT FILING DATE: 2000-02-15
; EARLIER APPLICATION NUMBER: 60/120,702
; EARLIER FILING DATE: 1999-February-19
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 256
; TYPE: PR
; ORGANISM: Brevibacterium sp HCU
US-09-504-358-14
Query Match 20.4%; Score 266; DB 4; Length 256;
Best Local Similarity 30.9%; Pred. No. 1.4e-21;
Matches 82; Conservative 39; Mismatches 116; Indels 28; Gaps 8;
QY 10 GLVAVITGASGLGLATAEERLVGQASAVLLDLPNSGGEQAQKL--GNNVVFAPADYV 66
; 6 KRAVAVITGGAAGMRIOSELYASEGAQVAVDVNEQEGRATADAIASGSGVANTYMLDVS 65
QY 67 SEKDVOATLALAKGKRGVADVAVNAGIAVASKTYNLKKQTHLE--DFQRYLDVNLG 124
; 66 DESEVELVSDIAKRGGAIVLVNAGVIGADK-----PTHEIDERDLVLSDVAG 118
Db 125 TFNVIRLVAGEMGQNEPDGQGGGVYIINTASVAAFEGOVQAASAKGIVGMLPIAR 184
; 119 VFEWTKRCIPYKQ---AGG--GAYVNFASIVGLVSOELPYHAAKGAVALITKODAV 172
QY 185 DIAPIGIRVMTIAPGLFETPLTSLPEKVCNFIASQVFPFSRLGDPAEV--AH 235
; 173 TYGSPNIRVNAVAPGIIITPLVLELSRGPDGIDGTTKLMGAKHPL--GRVGPDEEVAAT 231
QY 236 LVQAIENPFLNGEVIRLDGAIRMQ 260
; 232 LFLASEASFTIGAVLPVDSGYTAQ 256
Db 232 LFLASEASFTIGAVLPVDSGYTAQ 256
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RESULT 20
US-09-134-001C-4825
; Sequence 4825, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; LENGTH: 249
; TYPE: PRF
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4825

Query Match      20.9%; Score 272.5; DB 4; Length 249;
Best Local Similarity 29.1%; Pred. No. 2.5e-22;
Matches 74; Conservative 54; Mismatches 105; Indels 21; Gaps 6;

QY 13 AVITGASGLGATTAERLYVGOGASAVLLDLPNSGGEAQA-----KKGNNVVFAPADYTS 67
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 10 ALVYGASGIGRSALDLAEEGIN-VAVNTAGSKDKAEVVEETKACGVSPAIQAVAK 68
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 68 EKDVTOTALAKGFRGVAVNCAGIAVASKTYNLKGGQHTTLEDFQRYLDVNLGTFN 127
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 69 GDEVKEMKEVYVSGFSDVLYVNNAGITKDLIMRKE-----QEMDDVIDTILKGFVN 122
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 128 VIRLVASGEMGNEPDGGQGRVITINTASVAFEGOVGAAYASASKGIYGMTLPIARDLA 167
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 CIQKTPQMLRQ-----RSGAITNLTSIVGAMGNPQDANTYAKAGVIGITKAAMELA 176
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 188 PIGIRVMTIAPGLTGPLLTLSPKVCNFILASQVFPFSRLGDPRAEVAHLVQAITEN--PF 245
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 177 SRGITVNAVAPGFIYSDMTNLSDLDKQMLEQIPL-KRFGEDPIDANTVAFILASDRKXY 235
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 246 LMGVYIRLDGAIRM 259
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 236 ITGQTIHVNGGMYM 249
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 21
US-08-440-856A-3
; Sequence 3, Application US/08440856A
; Patent No. 5750873
; GENERAL INFORMATION:
; APPLICANT: DELAPORTA, STEPHEN L.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
; TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & ROEBSTER
; STREET: 2000 PENNSYLVANIA AVE. N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC Compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,856A
; FILING DATE: 15-MAY-1995

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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-3

Query Match      20.9%; Score 272.5; DB 1; Length 337;
Best Local Similarity 31.2%; Pred. No. 4e-22;
Matches 89; Conservative 44; Mismatches 111; Indels 41; Gaps 6;

QY 6 RSVKGLVAVITGASGLGATTAERLYVGOGASAVLLDLPNSGGEAQA-KKGNNVVFAPADY 65
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 51 KRLDGKVALVTGARGIGALYRLFAKRGARVYIDIDPAGELALASALGQVSPVRDXY 110
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 66 TSEKDVOTALAKGF-GRVDVAVNCAGIAVASKTYNLKGGQHTTLEDFQRYLDVNLG 124
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 111 SVEDDVRRADVALLSHGGRGLDYCNNGGV-LGRQTRARSLSPDAEFDFVRLVNLG 169
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 TENVIRLVASGEMGNEPDGGQGRVITINTASVAFEGOVGAAYASASKGIYGMTLPIAR 184
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 AALGMKAARAAAPR-----RAGSLVSVASVAAVUGGIPRAYTASHKHAITGLTKRNAAC 223
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 185 DLAPIGIRVMTIAPGLTGPLL-----TSLP-----EK 212
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 224 ELRAHGVAVNCVSPFVATPMLINMWRQGHDDATADRDLDLDVYVPSQVEKME 283
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 213 VCNFLASQVFPFSRLGDPRAEVAHLVQAITENPFLNGEYIRLDGAI 257
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 284 VVAGLTATLKGPTLRPDIAE-AVLFLASDEARTISGHNLVYDGV 327
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 22
US-09-134-4397
; Sequence 4397, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQUENCES: 14
; SEQ ID NO 4397
; LENGTH: 231
; TYPE: PRF
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4397

Query Match      20.6%; Score 269; DB 4; Length 231;
Best Local Similarity 33.3%; Pred. No. 5.4e-22;
Matches 66; Conservative 39; Mismatches 81; Indels 12; Gaps 2;

QY 8 VKGLVAVITGASGLGATTAERLYVGOGASAVLLDLPNSGGEAQA-KKGNNVVFAPADYTS 67
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DB 5 VKERVAVAVTGASGIGALINKLSQGSASTLVGRNEQRLNEIVQDLNPAKYVTADVY 64
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 68 EKDVTOTALAKGFRGVAVNCAGIAVASKTYNLKGGQHTTLEDFQRYLDVNLGTFN 127
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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FILING DATE: 13-AUG-1990  
APPLICATION NUMBER: 67,695  
FILING DATE: 29-JUN-1987  
SEQ ID NO: 4  
LENGTH: 273  
5512669-4

Query Match 21.7%; Score 282.5; DB 6; Length 273;  
Best Local Similarity 31.5%; Pred. No. 2,2e-23;  
Matches 90; Conservative 42; Mismatches 91; Indels 63; Gaps 11;

QY 12 VAVITGGASGLALAEALVGGASAVLDDLPNSGGEQAOKLGNVYFAA-----63  
DB 4 VALVTGGSGRGID-----AASIALKAAGYKVAASVAGDDAKFKKGTGIAV 51  
QY 64 ---DVTSEKDVOTALALAKKFGKRVDAVAVNCAGIYASKTYNLKKGTH--TLEDPOFVL 118  
DB 52 YKWDVSYEACVEGIAKYEADIGPDLVNNAGIT-----KDAFHKKTPPOQWAVI 103  
QY 119 DVNLKGTFRVY-----RLV-----AGEMQ-NEPDGQGR---GVILN 152  
DB 104 NTLNLGLFNMTHPVMSGMRSEFRIVNMISSINGQGMQANSVWSGMDRSGFRIVN 163  
QY 153 TASVAFEGOVGAAYASAKSGIYVMTLPIDIALPISIRWTIAPGLFTPLTSPDK 212  
DB 164 ISSINGQGMQGMQANYSAAKAGDGLFTALAGAKITVNAICPGYIGTEMVRAIPER 223  
QY 213 VCN-FLASQVFPSPRLGDPAEYAHV--QAIENFPLNGEVIRLDG 255  
DB 224 VNERIIPQIPY-GRLGEPDEIARIYVFLASDEAGFTIGTSISANG 268

RESULT 18  
US-09-134-001C-4431  
Sequence 4431, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: CTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 4431  
LENGTH: 274  
TYPE: PR  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4431

Query Match 21.4%; Score 278.5; DB 4; Length 274;  
Best Local Similarity 31.7%; Pred. No. 6,2e-23;  
Matches 83; Conservative 45; Mismatches 93; Indels 45; Gaps 8;

QY 12 VAVITGGASGLALAEALVGGASAVLDDLP-----NSGGEQAOKLGNVYFA 60  
DB 10 IAVITGASGTGGAGAAVALAIEGAHVLAIDSDLEETVQSIINDGGAATVAVR-----63  
QY 61 APADVTSKDVOTALALAKKFGKRVDAVAVNCAGIYASKTYNLKKGTH--TLEDPOFVL 118  
DB 64 ---DISDQYKQFSEKLAQEFGHADVIFENNAVDNGA-----GRHEYPVEYFDKIM 113  
QY 119 DVNLKGTFRVIRLVAVGEMGNEPDGQGRVYINTASVAFEGOVGAAYASAKSGIYGM 178  
DB 114 AVDMGTFVYKFL-----PLMKGGSLINTASFGAADIDRSGYNAAGVATNF 166  
QY 179 TLPIARDLAPIGIRWTIAPGLFTPL-----TSLPKVCNFTLASQ--VPPSPRLGPA 231  
DB 167 TKSIAIEYGRNIRANAIAPGIIETPLVDNLATGSDDEAGQTFRENCKWVPIGLRTGPD 226

QY 232 EYAHVQ--AIENPFLNGEVIRLDGAI 257  
DB 227 EVGKLVAFSLASDDSFITGETIRIDGV 254

## RESULT 19

US-08-858-207A-270  
Sequence 270, Application US/08858207A  
Patent No. 6348328  
GENERAL INFORMATION:

APPLICANT: Black, Michael  
APPLICANT: Hodgson, John  
APPLICANT: Knowles, David  
APPLICANT: Nicholas, Richard  
TITLE OF INVENTION: No. 6348328el Compounds  
NUMBER OF SEQUENCES: 552  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/858,207A  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/017670  
FILING DATE: 14-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmil, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50475  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 270:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 186 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6348328e  
US-08-858-207A-270

Query Match 20.9%; Score 273; DB 4; Length 186;  
Best Local Similarity 39.3%; Pred. No. 1,4e-22;  
Matches 75; Conservative 23; Mismatches 71; Indels 22; Gaps 5;

QY 15 ITGASGLALAEALVGGASAVLDDLPNSGGE-----AQAKKLGNNVYFPAVATSE 68  
DB 10 ITGSSRRIGALAHKFKQAQANIVL-----NSRGAISHELLAESNIGIKYVPIPSGVSDP 65  
QY 69 KDVOITALALAKKFGKRVDAVAVNCAGIYASKTYNLKKGTH--TLEDPOFVLVDNLKGTENV 128  
DB 66 ADARFMIDQAIIEAGSDVIVNNAGI--TODTLMKX---TEADDEKVLKYNLTGAFFM 119  
QY 129 IRLVAGMGNEPDGQGRVYINTASVAFEGOVGAAYASAKSGIYVMTLPIDIALP 188  
DB 120 TQSYL-----KPMKARBAEALINMSSVGLMGNIGQANTAAASKAGLIGTKVAAREVAS 173  
QY 189 IGIRVWTIAPG 199  
DB 174 RNIRVNIAPG 184

APPLICATION NUMBER: 08/562,114  
FILING DATE: 22-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/375,962  
FILING DATE: 20-JANUARY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/258,418  
FILING DATE: 10-JUNE-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 628097man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5372.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 838-3884  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase  
US-08-729-594A-13

Query Match 21.9%; Score 285.5; DB 4; Length 244;  
Best Local Similarity 29.6%; Pred. No. 8.5e-24;  
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLAVITGGASGLATRAELVGGASAVYLDLPNSGGEAKKLGNNVFAADVTSE 68  
DB 4 EKKIALVTGASRGIGRAIAETLAARGKVIATSENQAISIDYLGANGKGLMLNTDP 63  
QY 69 KDVOITALAKKGFGRVDVAVNCAGIAVASTYLNKKGOTHTLDFORVLDVNLKGTENV 128  
DB 64 ASIESVLEKRAEFGEVDILVNNAGITRDNLKMRKD-----DEWNDIETNLSVFR 117  
QY 129 IRLVAGMGONEPDGGRGVIIINTASVAAREGOVQAAYSASKGIVGMLPIARDLAP 188  
DB 118 SKAVRAMMKK-----RHRITITGSVGTMGNGQANYAAKAGLIGFSKSLAREVAS 171  
QY 189 IGIRVMTIADLGFPTLPLSLPEKVCNFLASQVPEPRLGDPAEYAHVQ--AIENPFL 246  
DB 172 RGIIVNVVAPGFETDTRALSDQDAGIILQVP-AGRLGAGQEIANAVAFASDEAYI 230  
QY 247 NGEVIRLDGAIRM 259  
DB 231 TGETLHVNGMYM 243

RESULT 16  
US-08-937-993-13  
Sequence 13, Application US/08937993  
Patent No. 639344

GENERAL INFORMATION:  
APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna  
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski L.L.P.  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,993

FILING DATE: September 26, 1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/729,594  
FILING DATE: 11-OCTOBER-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/562,114  
FILING DATE: 22-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 639344man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 838-3884  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase  
US-08-937-993-13

Query Match 21.9%; Score 285.5; DB 4; Length 244;  
Best Local Similarity 29.6%; Pred. No. 8.5e-24;  
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLAVITGGASGLATRAELVGGASAVYLDLPNSGGEAKKLGNNVFAADVTSE 68  
DB 4 EKKIALVTGASRGIGRAIAETLAARGKVIATSENQAISIDYLGANGKGLMLNTDP 63  
QY 69 KDVOITALAKKGFGRVDVAVNCAGIAVASTYLNKKGOTHTLDFORVLDVNLKGTENV 128  
DB 64 ASIESVLEKRAEFGEVDILVNNAGITRDNLKMRKD-----DEWNDIETNLSVFR 117  
QY 129 IRLVAGMGONEPDGGRGVIIINTASVAAREGOVQAAYSASKGIVGMLPIARDLAP 188  
DB 118 SKAVRAMMKK-----RHRITITGSVGTMGNGQANYAAKAGLIGFSKSLAREVAS 171  
QY 189 IGIRVMTIADLGFPTLPLSLPEKVCNFLASQVPEPRLGDPAEYAHVQ--AIENPFL 246  
DB 172 RGIIVNVVAPGFETDTRALSDQDAGIILQVP-AGRLGAGQEIANAVAFASDEAYI 230  
QY 247 NGEVIRLDGAIRM 259  
DB 231 TGETLHVNGMYM 243

RESULT 17  
5512669-4  
Patent No. 5512669  
APPLICANT: PROPLES, OLIVER P.; STINSKEY, ANTHONY J.  
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA  
REDUCTASE  
NUMBER OF SEQUENCES: 7  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,667  
FILING DATE: 29-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 124,570  
FILING DATE: 20-SEP-1993  
APPLICATION NUMBER: 944,488  
FILING DATE: 03-NOV-1992  
APPLICATION NUMBER: 566,535





RESULT 11  
US-08-793-035-10

Sequence 10, Application US/08793035  
Patent No. 6011301  
GENERAL INFORMATION:  
APPLICANT: Slabas, Antoni R.  
APPLICANT: White, Andrew  
APPLICANT: Chase, Diane  
APPLICANT: Elborough, Kelvin  
APPLICANT: Fentem, Phillip A.  
TITLE OF INVENTION: B-Ketacyl ACP Reductase Genes From  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,035  
FILING DATE: 28-JUL-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9414622.2  
FILING DATE: 20-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB95/01678  
FILING DATE: 17-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kammerer, Patricia A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: MOBT:132  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713.787.1440  
TELEFAX: 713.787.1440  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 315 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-793-035-10

Query Match 22.3%; Score 291; DB 3; Length 315;  
Best Local Similarity 30.5%; Pred. No. 3,1e-24;  
Matches 80; Conservative 44; Mismatches 116; Indels 22; Gaps 6;

QY 4 ACSRYGLAVITGSGGLTAEELVGGASAVLLDLPNSGGE---QAKRLGNV 58  
DB 66 AVPKVESPVYVTGASRGKALALSL-CKACKYLVNVAARKAEVSKQIEAYGGA 124  
QY 59 VEPADVTSEKDVQIALAKGKFGVDVAVNCAGIAVASKTYNLKKGOTHTLEDFQRYL 118  
DB 125 ITFGGVSKAEADVEAMKTAIDAWGITDVYVNNAGITRDTLLIRKKSQ-----WDEVI 178  
QY 119 DVNLMGTFFVIRLVAGMGONPEPDGGRGVITINTASVAEFGVQAAYSAKSGIYGM 178  
DB 179 DLNLTGVELCTQATITMKK-----RKGRIINLASVYGLIGNIGQANVAAKAGVIGF 232  
QY 179 TLEPIADLAPIGIRVMTIAPGLFTPLTSLPEKVCNPLASOVPPPSRIGDAEFAHLYQ 238  
DB 233 SKTAAREGASRNINNVAVCPGFIASDMTAKLEDMEKKITLITPL-GRAYGPEVDAVLVE 291  
QY 239 ALEENP---FLNGEVIRLDGAI 257

DB 292 FIALSPASYITGCAFTIDGI 313

RESULT 12  
5229279-7  
Patent No. 5229279  
TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER  
BIOPOLYMERS  
NUMBER OF SEQUENCES: 8  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/556,535  
FILING DATE: 13-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 67,695  
FILING DATE: 29-AUG-1987  
SEQ ID NO: 7  
LENGTH: 246  
5229279-7

Query Match 22.1%; Score 288.5; DB 6; Length 246;  
Best Local Similarity 31.9%; Pred. No. 4e-24;  
Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

QY 12 VAVITGGASGLTAEELVGGASAVLLDLPNSGGE---QAKRLGNVVPADVTS 67  
DB 5 IAYVTGGMGIGTALICQRLAKDGFVYAGGSPRRERWLEQKALGDFIASSEGNVAD 64  
QY 68 EKDVQIALAKGKFGVDVAVNCAGIAVASKTYNLKKGOTHTLEDFQRYLVNLMGTEN 127  
DB 65 WDSTKTFEDKVKSEVGEVDVLNNAGI---TROVERK---MTRADMDAVIDINTLSLEN 118  
QY 128 VIRLVAGMGONPEPDGGRGVITINTASVAEFGVQAAYSAKSGIYGMPLPIARDIA 187  
DB 119 VTKQVIDGMA---DRGM--GRIVNISVNGOKGQFQUTYSTAKAGLGFMAIAQEVA 172  
QY 188 PIGIRVMTIAPGLFTPLTSLPEKVCNPLASOVPPPSRIGDAEFAHLYQATII--ENPF 245  
DB 173 TKGVTAVTSPGTAIDMVAIRQVDIKIVATIPV-KRLGLPQELIASICAMLSSESGF 231  
QY 246 LNGEVIRLDGAIRM 259  
DB 232 STGADFSLNGILHM 245

RESULT 13  
US-08-375-962B-13

Sequence 13, Application US/08375962B  
Patent No. 5731195  
GENERAL INFORMATION:  
APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,  
TITLE OF INVENTION: Isolated Nucleic Acid Molecule  
TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol  
TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With F63,  
TITLE OF INVENTION: A Portion of a Retinol Binding Protein Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect (ASCII standard)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/375,962B  
FILING DATE: 20-January-1995  
CLASSIFICATION: 435

Query Match	22.6%	Score 295;	DB 4;	Length 263;
Best Local Similarity	32.3%	Pred. No. 8,2e-25;		
Matches	86;	Conservative	42;	Mismatches 104; Indels 34; Gaps 6;

  

QY	12	VAVITGASGSLGTAERLVGQASAVLLDLPNSCGEAOAKKL---	GNNVFAPADVYSE	68
Db	11	VAVVTGAAGGIGLKAERLFEDEGYSLAVDENEAAKSAESAKLSKEGEAAVAFKADVSNR		70
QY	69	KDVOTALAKGKFRGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFQRYLVANLNGSTENV		128
Db	71	DQVEFVLNQGVEHEDDLNVLVNNAAGLGPMTPI-----	ESVTPEDGFNQGVNVGAVFWEG	124
QY	129	IRLVAGEGQNEPDGGGQRGVLTINTASVAAPFGQVQAAYSASKSGIVSMTEPIARDLAP		188
Db	125	IOAAIEQF-----DLIGHGKLIINATSOAGVGNAGLSLSTKFAVRGLITVVAARDLAE		179
QY	189	IGIRVMTAPGLFGFPLLTSLPEKVCNFTASGVPPP-----	SRLDGPAEYA	234
Db	180	KNITVNAFAPGIVLPPPMKKGIAEK-----	LAENNQPMEMGWMKQFTQIALKRLSKPEDEVA	235
QY	235	HLVQAAIL--ENPFLNGEYTRLDGAIR		258
Db	236	NVVSFLAGSDSDYITGGTITIVDGMK		261

```

RESULT 9
US-09-363-189B-6
/ Sequence 6, Application US/09363189B
/ Patent No. 6242228
/ GENERAL INFORMATION:
/ APPLICANT: SUGIYAMA, MASAKAZU
/ APPLICANT: TONOUCHI, NAOTO
/ APPLICANT: SUZUKI, SHUNICHI
/ APPLICANT: YOKOZAKI, KENZO
/ TITLE OF INVENTION: XYLILOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
/ FILE REFERENCE: 0010-1024-0
/ CURRENT APPLICATION NUMBER: US/09/363,189B
/ CURRENT FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: JP10-216047
/ PRIOR FILING DATE: 1998-07-30
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.0
/ SEQ. ID NO 6
/ LENGTH: 262
/ TYPE: PRT
/ ORGANISM: Gluconobacter oxydans
/ US-09-363-189B-6

```

Query Match	Similarity	22.4%	Score 292.5	DB 4	Length 262
Best Local	Similarity 31.6%		Pred. No. 1.6e-24		
Matches	86	Conservative 41	Mismatches 110	Indels 35	Gaps 7
Qy	6	RSVKGIVAVITGASGLGATATERTLVGOGASVLLDLPNSG--GEAQAKKIGNNVFAP	62		
Db	3	KRFNGVVCVLTGAGGNGIGATATRLAEESTATALLDMNNEALEKAASVREKGVESRYV	62		
Qy	63	AVTSEKSDQVDTALALAKKGFGRVDVAVNCAGIAYASKTNLKKGTHTLEDPQRYVDNL	122		
Db	63	CVYTSEAVITGVYDSVYRDFPKIDFLFNNAVGOGA----FAPVQDYPPEDDARVLTINV	117		
Qy	123	MGTENVIRLVAGEM-GQNFEPDGGCGRGVLTINTASVAAEFGQYQAAISKSGIVMTLP	181		
Db	118	TCAFVHLKAVSRMOTIQN-----YGRIVNTASMAVGVPNNMAAYGASKGIALLTET	170		
Qy	182	IRADILAPIGIRVMTIAPGLF-----GPELTSILPEKVNFTLASQVFPES	225		
Db	171	ALDLAPYIRVIRVNAISPGYMGPGEMMERQVELQAKVGSQYFSTDPKRYAQQMGISVPM-R	229		
Qy	226	RLGDPREYIAHLVQAIT--ENPFLNGVITLDDG	255		
Db	230	RGVDINELPGVAVAFLLGGDSSFEFTGVNLTLAG	261		

```

RESULT 10
US-08-793-035-9
; Sequence 9, Application US/08793035
; Patent No. 6011201
; GENERAL INFORMATION:
; APPLICANT: Slabas, Antoni R.
; APPLICANT: White, Andrew
; APPLICANT: Chase, Dianne
; APPLICANT: Elborough, Keiran
; APPLICANT: Pentem, Phillip A.
; TITLE OF INVENTION: B-ketacyl ACP Reductase Genes From
; TITLE OF INVENTION: Brassica Napus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,035
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 800
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: GB 9414622.2
; FILING DATE: 20-JUL-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: GB95/01678
; FILING DATE: 17-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: M03T.132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-793-035-9

```

```

Query Match      22.3%; Score 291; DB 3; Length 315;
Best Local Similarity 30.5%; Pred. No. 3.1e-24;
Matches      80; Conservative 44; Mismatches 116; Indels 22; Gaps 6

QY      4 ACRSVKGLVAIVITGGASGIGLATAERLVQGSAAVLIDPNSGGEA----QAKLGNVY 58
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      66 AWPKEESPVVYVITGASRGIGKALALST--GKACKCVLVNARSARKEAEVYSKQIEAYGQOA 124
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      59 VVAPADVSEKVOVQATLAKGKFGVDDVAVNCAGIAVASKTYNLRKGGOTHLEDFQVYL 118
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      125 ITFGGDVSEADVEAMKRTAIDAKGIVDYVNNAGITRTLTILRMKKSQ-----WDEVI 178
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      119 DYNLKGTFENVIRLVAGSEMGQNEPDGQGRGVITINTASVAAFBQGOAAIYSASKGIVAK 178
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      179 DINTLGVFCTQOATKIMAKR-----RKGRITINIASVGLIGNIDQANVAAAKACAVIGF 232
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      179 TLPIARDLAPIGIRVVTIAPLGFGLFPLTSLPEKVYCNFLASQVFPFSRLGDPAPETVYAHLYQ 238
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      233 SKTAAREGASRNINNVVCPGFIASDMTKLLEDMEKRLTGLIPL--GRIGQEPEDVAGIWE 291
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      239 ATTEND--FLNGEVIKLDGAI 257
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      292 FLALSPRASYITGOAFTIDGCI 313
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Thu Jun 26 06:55:09 2003

us-09-931-186-6.ra1

Page 4

ADDRESS: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVE. N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,856A  
FILING DATE: 15-MAY-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A.  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 05463-20001.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1517  
TELEFAX: (202) 887-0763  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 333 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-440-856A-4  
Query Match 23.4%; Score 304.5; DB 1; Length 333;  
Best Local Similarity 32.9%; Pred. No. 1e-25;  
Matches 93; Conservative 46; Mismatches 105; Indels 39; Gaps 5;  
QY 6 RSVGLVAVITGASGGLATLAEKLVGGASAVLLDLPNSGGEQAOKLGNVYFADY 65  
DB 50 KRLBKVAVITGARGIGLAEVRLVFKHAKVVIADIDDAAGELALGPHEGVACDV 109  
QY 66 TSEKVOVALALAKGKFRVAVAVNCAGIAVASKTYNLKKGOTHTLDFQVLDVNLGT 125  
DB 110 SYEEVERAVERAARVGRIDVLCNNAGV-LGRQTPAKSLTSPDAGEFDEVLKVLGA 168  
QY 126 FNVITLVAGEKQNEPDGQGVYINTASVAEFGVGAAYASAGGIVGATLPARD 185  
DB 169 ALGKHAALAMTOR-----RAGSLISVAVAGVLGGLPHAYASKHAIKLNACE 222  
QY 186 LAPIGIRVMTAPGLFGTPLL-----TSLP-----EKVC 214  
DB 223 LGAGIRVNCISPFVATPMLINAKRGHDASTADADADIDDLIAYSDQEVKMEYV 282  
QY 215 NFASQVFPRLSDPAEYAHVQAIIENPFLNGEVIRLDGAI 257  
DB 283 RGLATLKGATLRPRDIAE-AALFLASDSDRYISGHNLVYDGV 324  
RESULT 7  
US-08-815-225-4  
Sequence 4, Application US/08815225  
Patent No. 6268479  
GENERAL INFORMATION:  
APPLICANT: Stern, David M.  
TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE  
TITLE OF INVENTION: BINDING (ERRA) POLYPEPTIDE AND METHODS FOR INHIBITING  
TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: U.S.A.

ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/815,225  
FILING DATE: 12-MAR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/55209  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-815-225-4  
Query Match 22.9%; Score 299; DB 4; Length 255;  
Best Local Similarity 33.6%; Pred. No. 2.8e-25;  
Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;  
QY 8 VGLVAVITGASGGLATLAEKLVGGASAVLLDLPNSGGEQAOKLGNVYFADY 67  
DB 4 LSKVYITGARGIGLAEVRLVFKHAKVVIADIDDAAGELALGPHEGVACDV 63  
QY 68 EKDVOVALALAKGKFRVAVAVNCAGIAVASKTYNLKKGOTHTLDFQVLDVNLGT 127  
DB 64 EEDMOWAVAYAKREFSVGLVNNACISTGML-----ETSEVERFRVYDINTLGVFI 117  
QY 128 FNVITLVAGEKQNEPDGQGVYINTASVAEFGVGAAYASAGGIVGATLPARD 187  
DB 118 GSKTVIPAM---KDGAG--GSLVINISSAAGLGLATLSYASGVNGSLKLAIVELG 171  
QY 188 PIGIRVMTAPGLFGTPLL-----TSLPEKVCNPLASQVPEPSRLG-DPAEYAHVQAIIIE-- 242  
DB 172 TDRIRVNSVHPKATYTPMAEIGIRGEGNY--PNTPM-GRVNGEGELAGAVVLLSDT 228  
QY 243 NPFLNGEVIRLDG 255  
DB 229 SSYVTGAEIAYDVG 241  
RESULT 8  
US-09-134-001C-4512  
Sequence 4512, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 4512  
LENGTH: 263  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4512

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES  
FILE REFERENCE: 2885-1651  
CURRENT APPLICATION NUMBER: US/09/347,878C  
CURRENT FILING DATE: 1999-07-06  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 50  
LENGTH: 261  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-347-878-50

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Best Local Similarity 99.6%; Pred. No. 4.2e-137;  
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 APADVTSEKDVQVATLAKKFGKRVDAVAVNCAGIAVASKTYNLKKGTHLEDFORVLDV 120  
OY 121 NLMGTFFNYRLVAGEMGNEPDGOGGVIIINTASVAFEGVQAAYSAKSGIYGMTL 180  
DB 121 NLMGTFFNYRLVAGEMGNEPDGOGGVIIINTASVAFEGVQAAYSAKSGIYGMTL 180  
OY 181 PIADLPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSRIGDAEYAHVQAI 240  
DB 181 PIADLPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSRIGDAEYAHVQAI 240  
OY 241 IENPFLNGEVRIDGAIKMP 261  
DB 241 IENPFLNGEVRIDGAIKMP 261

RESULT 4  
US-08-980-832-41  
Sequence 41, Application US/08980832B  
Patent No. 6291204  
GENERAL INFORMATION:  
APPLICANT: Tsyankov, Yuri  
TITLE OF INVENTION: Improved Fermentative Carotenoid Production  
FILE REFERENCE: Improved Fermentative Carotenoid  
CURRENT APPLICATION NUMBER: US/08/980,832B  
CURRENT FILING DATE: 1997-12-01  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 41  
LENGTH: 388  
TYPE: PRT  
ORGANISM: Flavobacterium sp. R1534  
US-08-980-832-41

Query Match 51.0%; Score 664.5; DB 4; Length 388;  
Best Local Similarity 55.5%; Pred. No. 7.2e-66;  
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

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DB 143 IEGRFVVTGASGLGASARMLAOGAKVYLDL-----AEPDADEGAVHAACDVT 196  
OY 68 EKDVOTATLAKKFGKRVDAVAVNCAGIAVASKTYNLKKGTHLEDFORVLDVNLGTFN 127  
DB 197 ATAAATATATADRGRDGLVNCAGIAPEERM--LGNDGPHGLDPSFARATINLISFN 254  
OY 128 VIRLVAGEMGNEPDGOGGVIIINTASVAFEGVQAAYSAKSGIYGMTLPIARDA 187  
DB 255 MARLAEMARNEPVR-GERGVIVTASTIAODGQIGVAVAAASKAGVAGMTLPMARDA 313  
OY 188 PIGIVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSRIGDAEYAHVQAIENPFLN 247

DB 314 RHGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSRIGDAEYAHVQAIENPFLN 373  
OY 248 GEVIRIDGAIKMP 261  
DB 374 GEVIRIDGAIKMP 387

RESULT 5  
US-09-239-052-2  
Sequence 2, Application US/09239052  
Patent No. 6346395  
GENERAL INFORMATION:  
APPLICANT: Holmes, David J.  
APPLICANT: Zhong, Yixi  
APPLICANT: Debouck, Christine  
APPLICANT: Jaworski, Deborah D.  
APPLICANT: Wang, Min  
APPLICANT: Warren, Richard L.  
APPLICANT: Kosmatka, Anna L.  
APPLICANT: McDevitt, Damien  
APPLICANT: Ingraham, Karen A.  
APPLICANT: Chalke, Allison F.  
APPLICANT: So, Chi Young  
APPLICANT: Wallis, Nicola G.  
APPLICANT: Pearson, Stewart C.  
TITLE OF INVENTION: Fads  
FILE REFERENCE: GMI0191  
CURRENT APPLICATION NUMBER: US/09/239,052  
CURRENT FILING DATE: 1999-01-27  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-09-239-052-2

Query Match 25.4%; Score 331.5; DB 4; Length 243;  
Best Local Similarity 35.5%; Pred. No. 6e-29;  
Matches 89; Conservative 36; Mismatches 103; Indels 23; Gaps 6;

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DB 10 ITSSRSRIGLAIHKEFAQAGANIVL-----NSRGAISELLAERSNYGIKVPISGVDF 65  
OY 69 KDVTATLAKKFGKRVDAVAVNCAGIAVASKTYNLKKGTHLEDFORVLDVNLGTFN 128  
DB 66 ADKRMIDQAIIEIGSDVAVNNAGI--TQDTMLCK---TADFEKVLKVLTAEFNK 119  
OY 129 IRLVAGEMGNEPDGOGGVIIINTASVAFEGVQAAYSAKSGIYGMTLPIARDA 188  
DB 120 TQSVL-----KMKMRREGAIIIMSSVAGLMGNIGANAAKAGLIGFTKSVAREVA 173  
OY 189 IGRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSRIGDAEYAHVQAIENPFLN 248  
DB 174 RNLRVNIAAGMESDITAILSDIKETALQIEM--KEGQABQVADLTVELAGQDYLIG 232  
OY 249 EVIRIDGAIKMP 259  
DB 233 QVIAIDGGLSM 243

RESULT 6  
US-08-440-856A-4  
Sequence 4, Application US/08440856A  
Patent No. 5750873  
GENERAL INFORMATION:  
APPLICANT: DELAPORTA, STEPHEN L.  
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

## ALIGNMENTS

## RESULT 1

US-08-815-225-2

; Sequence 2, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper &amp; Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-815-225-2

Query Match 99.6%; Score 1299; DB 4; Length 261;  
Best Local Similarity 99.6%; Pred. No. 4.2e-137;  
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MAACRSYKGLVAVITGASGLGLATAERLVGOGASAVLLDLPNSGGEQAQKLGNNVF 60
QY 61 AAPVTSKDVQVOTLALAKGKFGVDVAVNCAGIAVASKTYNKKGGOTHTLEDFORLDV 120
DB 61 AAPVTSKDVQVOTLALAKGKFGVDVAVNCAGIAVASKTYNKKGGOTHTLEDFORLDV 120
QY 121 NLMGFNVIRLVAGEMGNEDDGGGQGVIIINTASVAAPFEGVGOAAYSASKGIYGMTL 180
DB 121 NLMGFNVIRLVAGEMGNEDDGGGQGVIIINTASVAAPFEGVGOAAYSASKGIYGMTL 180
QY 181 PIARDLAPIGIRVMTIAPGLFGTPLLTLSPKVCNFIASQVPPPSRLGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFGTPLLTLSPKVCNFIASQVPPPSRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIRMOP 261
DB 241 IENPFLNGEVIRLDGAIRMOP 261
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RESULT 2

## US-08-815-225-3

; Sequence 3, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper &amp; Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-815-225-3

Query Match 99.6%; Score 1299; DB 4; Length 261;  
Best Local Similarity 99.6%; Pred. No. 4.2e-137;  
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MAACRSYKGLVAVITGASGLGLATAERLVGOGASAVLLDLPNSGGEQAQKLGNNVF 60
QY 61 AAPVTSKDVQVOTLALAKGKFGVDVAVNCAGIAVASKTYNKKGGOTHTLEDFORLDV 120
DB 61 AAPVTSKDVQVOTLALAKGKFGVDVAVNCAGIAVASKTYNKKGGOTHTLEDFORLDV 120
QY 121 NLMGFNVIRLVAGEMGNEDDGGGQGVIIINTASVAAPFEGVGOAAYSASKGIYGMTL 180
DB 121 NLMGFNVIRLVAGEMGNEDDGGGQGVIIINTASVAAPFEGVGOAAYSASKGIYGMTL 180
QY 181 PIARDLAPIGIRVMTIAPGLFGTPLLTLSPKVCNFIASQVPPPSRLGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFGTPLLTLSPKVCNFIASQVPPPSRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIRMOP 261
DB 241 IENPFLNGEVIRLDGAIRMOP 261
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## RESULT 3

US-09-347-878-50

; Sequence 50, Application US/09347878C

; Patent No. 6376210

; GENERAL INFORMATION:

; APPLICANT: Yuan, Chong

Thu Jun 26 06:55:09 2003

us-09-931-186-6.rat

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:24:27 ; Search time 12.1667 Seconds

(without alignments)  
631.182 Million cell updates/sec

Title: US-09-931-186-6

Perfect score: 1304

Sequence: 1 MAACRSYKGLAVITGAS.....ENPLNGEVIIRLDGAIKMP 261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 100 summaries

Database :

1: /cgn2\_6/prodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1299	99.6	261	4	US-08-815-225-3
3	1299	99.6	261	4	US-09-347-878-50
4	664.5	51.0	388	4	US-08-980-832-41
5	331.5	25.4	243	4	US-09-239-052-2
6	304.5	23.4	333	1	US-08-440-856A-4
7	299	22.9	255	4	US-08-815-225-4
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77	169.5	13.0	317	4	US-08-729-584A-37
78	169.5	13.0	317	4	US-08-937-993-37
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80	163.5	12.5	319	2	US-08-977-847-1
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84	162.5	12.5	317	4	US-08-940-424-5
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88	161.5	12.4	335	3	US-09-002-298-7
89	159.5	12.2	316	4	US-08-729-594A-36
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91	159.5	12.2	316	4	US-08-940-424-2
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93	156.5	12.0	335	3	US-09-109-205-19
94	154.5	11.8	317	2	US-08-977-847-3
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96	154.5	11.8	317	4	US-08-940-424-4
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98	154	11.8	318	4	US-09-439-313-339
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.3%; Score 290.5; DB 9; Length 270;

Best Local Similarity 31.7%; Pred. No. 4.2e-18; Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

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DB 1 MATGR-YAKRYVYVYGGGRCIGAGIVRAFNAGAVYICDDESGRLBEL-PGAVF 58  
QY 61 APADVTSEKDVOTALALANGKFGKRDVAVNCAIGIAVASTYKMKQGHTLEDFOQVLDV 120  
DB 59 IICDVTQEDDVKTIVSETIRFRGLDCVNNAGHPP-----QREETSAGGFOLLEL 113  
QY 121 NLMGTFNVIRLVAGEGONEDPDGGRGYIINTASVAATEGGVGAAYASAGGIYGMTL 180  
DB 114 NLGITTTLTKLALPYRKSD-----GNVINISLVGALGQANAPYATGATYAMTK 166  
QY 181 PIARDIAPIGIRVMTIAPGLFGTPLLTSLEPKYCNFLASQVPP-----STL 227  
DB 167 ALALDESFGVRVNCISPGNIWPLWEE-----LAALMDPRATIREGMLAOLPGM 218  
QY 228 GDPAEY-AHLYQAIENPFLNG-EVIRLDGA 256  
DB 219 GDPAEYGAANVFLASEANFCTGIELLVGTGA 249

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Query Match 22.3%; Score 290.5; DB 9; Length 270;  
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Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

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OY 61 APADYSEKDVQALALAKKFEGRVDVAVNACIAVASKTYNKKGQTHLEDFQRYLDV 120  
DB 59 ILICVTGEDDVKTIVSEIRIRFGRDCVYNNAGHHPP-----ORPETSAQGFROLLEL 113  
OY 121 NLMGTFNVRFLVAGEMGNEDPGGQGVIIINTASVAFGQVQAAVSASKGIVMTL 180  
DB 114 NLGTYITRLKALYLRKSO-----GNVINISLVGALGQAAVYVAFKQAVTMTX 166  
OY 181 PIADLAPIGIRVWTIAPGLFGLTLSPKVCNFIASQVPP-----SRL 227  
DB 167 ALADESPYGVKVCISGNIWPLWE-----LAALMPDRATIREGMLAQPLGRM 218  
OY 228 GDPAEY-AHLVQAIENFPLNG-EVIRLDGA 256  
DB 219 GQPAEYGAAYFLASEANFCIGIELLYTGGA 249

RESULT 25  
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Sequence 468, Application US/09978192A  
Patent No. US20020177553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavich, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
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PRIOR FILING DATE: 2001-07-30  
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Query Match 22.3% Score 290.5; DB 9; Length 270;  
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Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

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DB 1 MATGR-YAGKVVVYVGGGRCIGAGIVAFVNSGARVVICDXDESGRALEQEL-PGAVF 58  
QY 61 APADVSEKDVQATLAKKFGADVAVVACAGIAVASKYNNLKKQTHLEDFORLAV 120  
DB 59 ILCDVTEDDVKTLVSETIRFRRLDCVNNASHRRP-----QREETSAGCFRLLEL 113  
QY 121 NLMTFNVIRLVAGEMQNEPDGQGVLIINTASVAEFGVGAAYASAKGIVGML 180  
DB 114 NLGTYFLTLALPYLRSQ-----GNVINISLVGALGQAVPYATKAVTAMRK 166  
QY 181 PIADLAPICIRWTIPGFGTPLTSLPEKCNFLASGVPP-----SRL 227  
DB 167 ALALDESPYGVVNCISPGNIMPLMBE-----LAALPDPRAITREGMIAQLGRK 218  
QY 228 GDPAEV-AHLVQAITEPNFLNG-EVIRLDGA 256  
DB 219 GQPAEVGAAVFLASEANFCTGIELLYTGA 249

RESULT 24  
US-09-978-697-468  
Sequence 468, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowskl, Paul J.  
APPLICANT: Gimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillap, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paonli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunes, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978, 697

ORGANISM: Gluconobacter oxydans  
US-09-802-853-6

Query Match 22.4% Score 292.5; DB 10; Length 262;  
Best Local Similarity 31.6% Pred. No. 2.7e-18;  
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

QY 6 RSVKLVAVITGSGAGLTAERLVGQASAVLIDPNSG---GEAQAQKLGNNVFAP 62  
DB 3 KRFNKKVCLVYGAGNIGLALALRAEGRGTAALDDMMRELKAEASVREKGYEASVY 62  
QY 63 ADVTSKDVQALALAKKRGFVDVAVNAGIAVASKYNNKKQGTHTLEDFQVLDVNL 122  
DB 63 CDVTSEAVIGTVDSVDFPKIDFLFNNAGYOGA----FAPVQDYPSDDFAFVLTINV 117  
QY 123 MGTENVITLVAGEM-GQNEPQGGGQGVYITNTASVAFEGOVGOAAVSASKGIVGMLP 181  
DB 118 TGAFTVLKAVSKQMTQN-----YGRIVNTASAGVKGPPNMAAYGASGAILTLET 170  
QY 182 IARDLAPIGIRVMTAPGLF-----GTPILTSLEKYCNFLASQVPPPS 225  
DB 171 AALDLAPYIRVNAISPGMGPFMRQVELQAKVGSQYFSTDPKVVAAQMGISVPM-R 229  
QY 226 RLGDPAEYAHLYQAI--ENPFLNGEVIRLDG 255  
DB 230 RYGDINEIRGVVAFLIGDDSSFTMGVNLPIAG 261

RESULT 23  
US-09-978-295A-468  
Sequence 468, Application US/09978295A  
Patent No. US2002015606A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
CURRENT FILING DATE: 2001-10-15  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819

Thu Jun 26 06:55:09 2003

us-09-931-186-6.rapb

Page 10

TYPE: PRT  
ORGANISM: Bacillus megaterium  
US-09-479-040-9

Query Match 23.1%; Score 301; DB 9; Length 247;  
Best Local Similarity 29.1%; Pred. No. 4,4e-19;  
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

7 SVKGLVAVITGASGLATAEERLVGCG-----ASAVLLDPNSGGEQAOK 53  
3 TLQKVAIVTGSGLGIAITRELSNGVAVANNYSKESABAIYEIKDNGEA---- 58  
54 LGNNVAPADYSEKIDVOTALAKKREGRVAVNACIAVASKTYNKK-GCHITL 112  
59 ----IAVQADVSVDOAKHLIETKAFQDLIVNNAI---TRDRSKKLGE-----E 106  
113 DFOHLDVNLMTFNVIRLVAGENGQNEPDGQGVINTASVAEFGVQQAAYSASK 172  
107 DMKVIDVNLHSVNTSALTLHLESE---GGR---VINISSIGAGFGQNTYSAK 160  
173 GGIVGMLPIARDLAPIGIRMTIAPGLFTPLLSPEKVCNFIASQVFPBRIDPAP 232  
161 AGMLGFKSLALELAKGVYNAICPGFIETEMVAIPEDVRAKIVAKIP-TRILGHAE 219  
233 YAH-LVQAIIENPFLNGEVIRLDGAIRM 259  
220 IARGVVIKAGCAIITGQOLNINGLYM 247

RESULT 20  
US-09-773-748-1  
Sequence 1, Application US/09773748  
Publication No. US20020187537A1  
GENERAL INFORMATION:  
APPLICANT: Wada, Masaru  
TITLE OF INVENTION: Levodione reductase gene and use thereof  
FILE REFERENCE: Levodione reductase  
CURRENT APPLICATION NUMBER: US/09/773,748  
CURRENT FILING DATE: 2001-01-31  
PRIOR APPLICATION NUMBER: EP00101665.8  
PRIOR FILING DATE: 2000-02-01  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn ver. 2.1  
SEQ ID NO 1  
LENGTH: 267  
TYPE: PRT  
ORGANISM: Corynebacterium aquaticum  
US-09-773-748-1

Query Match 22.8%; Score 297.5; DB 9; Length 267;  
Best Local Similarity 31.8%; Pred. No. 9.9e-19;  
Matches 84; Conservative 46; Mismatches 97; Indels 37; Gaps 9;

12 VAVITGASGLATAEERLVGASAVLLDPNSGGEQAOKL-----GNNVYAPADYT 66  
15 VLVITGSGGLRATAVRLAAGAKLSIVDSSEGLASKAIVLETAPDAVELTVAVDS 74  
67 SKDVQOTALAKKFGFRVDVAVNAGIAVASKITNKKQTHLEDPQVILDVNLMT 126  
75 DDAQVAVYVATTEFRIDGFFNNAGLEBKO-----NPTSEFTAEEDKVVSLRGVF 129  
127 ----VIVRLVAGEMQNEPDGQGVINTASVAEFGVQQAAYSASKGIYGMTLPI 182  
130 LQLEVLAKIMR-----EGGS--GMVYNTASVGINGIGNSGYAAAKHGVGLTRNS 179  
183 AADLAPIGIRMTIAPGLFTPLLSL-----PEKVC-NFLASQVFPBRIDPAP 233  
180 AVEYGRYGRIRINAVGALVMTPEVNSMKOLDPENPRKAAEEFI--QVNPSPKRYEAP 237  
234 AHIYQAIEN--PFLNGEVIRLDG 255  
238 AAVVAFLLSDASVYNAIVTPIDG 261

RESULT 21  
US-10-307-385-6  
Sequence 6, Application US/10307385  
Publication No. US20030077979A1  
GENERAL INFORMATION:  
APPLICANT: SUGIYAMA, MASAKAZU  
APPLICANT: TONOUCHI, NAOTO  
APPLICANT: SUZUKI, SHUNICHI  
TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF  
FILE REFERENCE: 0010-1024-0  
CURRENT APPLICATION NUMBER: US/10/307,385  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: US/09/363,189  
PRIOR FILING DATE: 1998-07-26  
PRIOR FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 262  
TYPE: PRT  
ORGANISM: Glucobacter oxydans  
US-10-307-385-6

6 RSVKGLVAVITGASGLATAEERLVGQASAVLLDPNSG---GEQAOKXIGNNVAP 62  
3 KKEGKVCVLTGAGNIGATLRLAEESTALALDMNEALKEKASVREKVEARSTV 62  
63 ADVSEKDVOTALAKKFGFRVDVAVNAGIAVASKITNKKQTHLEDPQVILDVNL 122  
63 CVTSEAVVIGTDSVVRDEFGKIDFLFNAGVGA-----FAPVODYPEDDFARVLTIV 117  
123 MGFNVIRLVAGEM-QONEPDGQGVINTASVAEFGVQQAAYSASKGIYGMTLP 181  
118 TGAFHVILKAVSRQIMON-----YGRIVNTASMGVGRPPMAAYGASKAIIALTET 170  
182 IARDLAPIGIRMTIAPGLF-----GTPILSLPEKVCNFIASQVFP 225  
171 AADLAPYINRVAIAISPGVGPFGFMERQVELQAKVGSQVFSFDPVAVQOMIGVPM-R 229  
226 RLGDPAEYAHVQAII--ENPFLNGEVIRLDG 255  
230 RYGDINEIPGVAVFLLGDSSFMTGVNLP 261

Query Match 22.4%; Score 292.5; DB 9; Length 262;  
Best Local Similarity 31.6%; Pred. No. 2.7e-18;  
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

US-09-802-853-6  
Sequence 6, Application US/09802853  
Patent No. US20010034049A1  
GENERAL INFORMATION:  
APPLICANT: SUGIYAMA, MASAKAZU  
APPLICANT: TONOUCHI, NAOTO  
APPLICANT: SUZUKI, SHUNICHI  
TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF  
FILE REFERENCE: 0010-1024-0  
CURRENT APPLICATION NUMBER: US/09/802,853  
CURRENT FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: 09/363,189  
PRIOR FILING DATE: 1998-07-29  
PRIOR APPLICATION NUMBER: JP10-216047  
PRIOR FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 262  
TYPE: PRT

OY 247 NGEYIRLDGATRM 259  
Db 223 TGHVLYVDGGLQI 235

## RESULT 17

US-09-815-242-10921  
Sequence 10921, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlssen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
TITLE OF INVENTION: Prokaryotes  
FILE REFERENCE: EUTRA-0114  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 10921  
LENGTH: 245  
TYPE: PR1  
ORGANISM: Enterococcus faecalis  
US-09-815-242-10921

Query Match 23.7%; Score 308.5; DB 10; Length 245;  
Best Local Similarity 33.3%; Pred. No. 9.3e-20;  
Matches 83; Conservative 38; Mismatches 109; Indels 19; Gaps 5;

OY 15 ITGASGSLGATAEHLVGGASAVLDD---LPNSGGGAQAKKIGNNVFAPADVTSEKD 70  
Db 10 ITGSTRGIGKAVLAFAKEGAIYVINGSEITPEQROETEA--FGVKCIGISGDISPDA 67  
OY 71 VOTALAKKGRFGRVAVANCAGIAVASKTYNLKKQHTLEDFORVLDVNMGTENVIR 130  
Db 68 AGEMIOATVDDQSIDILVNNAGIT-----NDKLLTMTKEDFACIDIMLVGTFNNQI 121  
OY 131 LVAGMGONEDPDGGRGVIIINTASVAPEGOVGOAASASAKGIVGTELTARDIAPIG 190  
Db 122 QAVKRMQ-----RSRITIMASVSGLMGVGANTYASRAGVGTKSVAREVAPRG 175  
OY 191 IRVMTIAPGLFTPLLTSLPEKVCNFTLASOVPFESRLDDPAEYAHVQAIIENPFLNGEV 250  
Db 176 ITCNALADPGIQTETMTDVLSERVKTKOMNAQIPLGT--FGQVBDVATAIFLAKSPYITGOV 234  
OY 251 IRLDGAIRM 259  
Db 235 VAVDGLVAV 243

RESULT 18  
US-09-931-186-15  
Sequence 15, Application US/09931186

Patent No. US20020132319A1  
GENERAL INFORMATION:  
APPLICANT: ABREO, MELWYN A.  
APPLICANT: ABREO, CHARLES S.  
APPLICANT: AUST, ROBERT  
APPLICANT: KISSINGER, CHARLES R.  
APPLICANT: MARGOSIAK, STEVE  
APPLICANT: MENG, JERRY J.  
APPLICANT: PELLETIER, LAURA A.  
APPLICANT: REUTO, PAUL A.  
APPLICANT: SHOWALTER, RICHARD E.  
APPLICANT: TEMPCZYK-RUSSELL, ANNA  
APPLICANT: THOMSON, JIM  
APPLICANT: VANDERPOOL, DARIN  
APPLICANT: VILLAFRANCA, J. ERNEST  
TITLE OF INVENTION: PEPTIDE MOTIF OF HUMAN ERAB/RAD2, ITS X-RAY CRYSTAL  
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION  
TITLE OF INVENTION: OF INHIBITORS THEREOF  
FILE REFERENCE: 0125-0049  
CURRENT APPLICATION NUMBER: US/09/931,186  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 15  
LENGTH: 253  
TYPE: PR1  
ORGANISM: Streptomyces hydrogenans  
US-09-931-186-15

Query Match 23.4%; Score 305.5; DB 10; Length 253;  
Best Local Similarity 33.3%; Pred. No. 1.8e-19;  
Matches 84; Conservative 48; Mismatches 101; Indels 19; Gaps 7;

OY 8 VKGLVAVITFGASGLIATAEHLVGGASAVLDDLPNSGGGAQAKKIGNNVFAPADVTSEKD 67  
Db 3 LSKRTYIITIGGAGLGEARQAQVAGARVLDVDEGAATARELGDAARQHDVYI 62  
OY 68 EKDVOTALAKKGRFGRVAVANCAGIAVASKTYNLKKQHTLEDFORVLDVNMGTENVIR 127  
Db 63 EEDMORVAVAREFSSVDGLVNNAGISTGMFL-----ETESVERFRVVEINLVGVI 116  
OY 128 VIRLVAGMGONEDPDGGRGVIIINTASVAPEGOVGOAASASAKGIVGTELTARDIAPIG 187  
Db 117 GKTIVIPAM---KDGAG--GSIVNLSAAGLGLATLSYKSKGVGSLKLAIVEIG 170  
OY 188 PIGIRVMTIAPGLFTPLLTSLPEKVCNFTLASOVPFESRLDDPAEYAHVQAIIENPFLNGEV 243  
Db 171 TDIRVNSVVRGKMTVPMETGTIRGEGNY--PNTPM--GRVGPGLIAGAVVKKLLSDTS 227  
OY 244 PFLNGEYIRLDG 255  
Db 228 SYVIGAEIAYDG 239

## RESULT 19

US-09-479-040-9  
Sequence 9, Application US/09479040  
Publication No. US20020182690A1  
GENERAL INFORMATION:  
APPLICANT: MCCOOL, Gabriel J.  
APPLICANT: Cannon, Maura C.  
APPLICANT: Cannon, Francis C.  
APPLICANT: Valentin, Henry E.  
APPLICANT: Gruys, Kenneth J.  
TITLE OF INVENTION: POLYHYDROXYALKANATE BIOSYNTHESIS ASSOCIATED PROTEINS  
TITLE OF INVENTION: AND CODING REGION IN BACILLUS MEGATERIUM  
FILE REFERENCE: M0B1212  
CURRENT APPLICATION NUMBER: US/09/479,040  
CURRENT FILING DATE: 2000-01-07  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 9  
LENGTH: 247



```

; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, MELVYN A.
; APPLICANT: AGREE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISTINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMCZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-931-186-17

Query Match      25.5%; Score 332.5; DB 10; Length 259;
Best Local Similarity 31.2%; Pred. No. 7,4e-22;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;

QY      8 VAGLVAVITGASGIGLTAERLVGOGASAVLDDLPNSGGEQAKL-----GN 56
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      7 LNSALALVYGAGSGIGRAVSVRLAGEGATVAAACDIDRAAOGETVRLGPGSGKEGPPRGN 66
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      57 NVYFAPADVTSEKDVOTALALAKKFRGR-VDYAVNCAAGIAVASKTYNKKGQTHLTLEDFQ 115
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      67 HAAF-QADVSEARARACLLLEQVQACFSRPSVYVSCAGITODEFLHSE-----DDWD 119
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      116 RYLDVNLKGTENVITLVAGGCONEPDGGGQGVYINTASVAAFEQGVGOAAYSASKSGI 175
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      120 KYIAVNLKGTFLYTAADALVSN-----GCRGSIINISITGKVGNGQGVYAAASKGV 174
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      176 VGMTPLIARDLAPIGIRVITAPGLFGLTSLPEKCNFLASQVPPSRIGDPAEYAH 235
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      175 IGLTQTAARELGRHGRCHRSVLPGLATPMTOKVQKVDKITEMIPM-GHIGDEEDVAD 233
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      236 LVQ--AIENPFLNGEVIRLDGAIKM 259
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      234 VVAFLASEDSGYITGTSTVEVTGLPM 259
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13
US-09-815-242-13360
; Sequence 13360, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078

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; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13360
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-815-242-13360

Query Match      25.4%; Score 331.5; DB 10; Length 243;
Best Local Similarity 35.5%; Pred. No. 8,4e-22;
Matches 89; Conservative 36; Mismatches 103; Indels 23; Gaps 6;

QY      15 ITGASGLGATARLVGOGASAVLDDLPNSGE-----AQAKKIGNNVYFAPADVTSE 68
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      10 ITGSSRGIGLAIARKEAQAANIVL---NSRGAISELLAEFSNGIKVPIGSDVDF 65
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      69 KDVTOTALAKKGRGVAVVAVNCAGIAVASKTYNKKGQTHLTLEDFQRYLDVNLKGTENV 128
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      66 ADARIMDQIAELGSDVLYVNNAGI--TQDTLTKM---TEADFEKVLKVLGAFNM 119
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      129 IRVAVGEGONEPDGGGQGVYINTASVAAFEQGVGOAAYSASKSGIYGVNLTPLARDLAP 188
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      120 TQSVL-----KPMKARKEGAILNMSSVGLMGIGQANTPAASAGLIGFTKSAREVAS 173
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      189 IGIRVMTIAPGLFGLTSLPEKCNFLASQVPPSRIGDPAEYAHVQAIIENPFLNG 248
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      174 RNIVNVNAPBMISDMWTALISDKIKETLAQIPM-KEFGQAEQVADLVTFLAGQDYLTG 232
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      249 EYIRLDGAIKM 259
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      233 QVIAIDGGLSM 243
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 14
US-09-815-242-13581
; Sequence 13581, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-966-245

Query Match
Best Local Similarity 99.6%; Pred. No. 3, 2e-93;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAVLLDLPNSGGEGAAKRLGNNVVFAPADVTSEKDVOTATLAKKRGVDAVNCAGI 94
DB 1 ASAVLLDLPNSGGEGAAKRLGNNVVFAPADVTSEKDVOTATLAKKRGVDAVNCAGI 60
QY 95 AVASKTYNLKKGQTHLEDFQRYLDVNLMTGFNVIRLVAGEMGONEPDGGRGVIIINTA 154
DB 61 AVASKTYNLKKGQTHLEDFQRYLDVNLMTGFNVIRLVAGEMGONEPDGGRGVIIINTA 120
QY 155 SVAAFEGVGQAAYASASKSGIGVMTLPARDLAPIGIRVMTIAPGLFETPLTSLPERVC 214
DB 121 SVAAFEGVGQAAYASASKSGIGVMTLPARDLAPIGIRVMTIAPGLFETPLTSLPERVC 180
QY 215 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKROP 261
DB 181 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKROP 227

RESULT 10
US-10-143-090-245
; Sequence 245, Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 245
; LENGTH: 227
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-143-090-245

Query Match
Best Local Similarity 87.1%; Score 1136; DB 9; Length 227;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAVLLDLPNSGGEGAAKRLGNNVVFAPADVTSEKDVOTATLAKKRGVDAVNCAGI 94
DB 1 ASAVLLDLPNSGGEGAAKRLGNNVVFAPADVTSEKDVOTATLAKKRGVDAVNCAGI 60
QY 95 AVASKTYNLKKGQTHLEDFQRYLDVNLMTGFNVIRLVAGEMGONEPDGGRGVIIINTA 154
DB 61 AVASKTYNLKKGQTHLEDFQRYLDVNLMTGFNVIRLVAGEMGONEPDGGRGVIIINTA 120
QY 155 SVAAFEGVGQAAYASASKSGIGVMTLPARDLAPIGIRVMTIAPGLFETPLTSLPERVC 214
DB 121 SVAAFEGVGQAAYASASKSGIGVMTLPARDLAPIGIRVMTIAPGLFETPLTSLPERVC 180
QY 215 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKROP 261
DB 181 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKROP 227

RESULT 11
US-09-920-923-41
; Sequence 41, Application US/09920923
; Publication No. US2003002273A1
; GENERAL INFORMATION:
; APPLICANT: Tsigankov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US/09/920,923
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 41
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Flavobacterium sp. R1534
US-09-920-923-41

Query Match
Best Local Similarity 51.0%; Score 664.5; DB 9; Length 388;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITGASGLGATAEERLVGGASAVLLDLPNSGGEGAAKRLGNNVVFAPADVT 67
DB 143 IEGRVFVVTGAASGLGASARMLAQGAKVLADEL-----ABPKAPPGAVHAACDVT 196
QY 68 EKQVQNALAAKRFGRVDAVNCAGIYASKTYNLKKGQTHLEDFQRYLDVNLMTGFN 127
DB 197 ATAAQTAIALATBFGDLGVNCAGIAPAEKRY--LGRGPRGLDSFAVAATINLIGSN 254
QY 128 VIRLVAGEMGONEPDGGRGVIIINTASVAAFEGVGQAAYASASKSGIGVMTLPARDIA 187
DB 255 MARLAEAAMARNEPVR-GERGVIVNTASIAACGCGOVAYASAKGAVGMLPMARDIA 313
QY 188 PIGIRVMTIAPGLFETPLTSLPERVCNPLASQVPPPSRLGDPAEYAHVQAIIENPFLN 247
DB 314 RHGIRVMTIAPGLFETPLTSLPERVGLPDVDSDLGAAVPPPSRLGEPSEYAAALHIIIPMLN 373
QY 248 GEVIRLDGAIKROP 261
DB 374 GEVIRLDGAIKROP 387

RESULT 12
US-09-931-186-17
; Sequence 17, Application US/09931186
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Page 5

Best Local Similarity 99.6%; Pred. No. 3.2e-93;  
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 35 ASAYLLDLPNSGGGAQAKKLGNNVVFAPADVTSEKDVQTALALAKGFGYDVAVNCAGI 94
    |||||
DB 1 ASAYLLDLPNSGGGAQAKKLGNNVVFAPADVTSEKDVQTALALAKGFGYDVAVNCAGI 60
QY 95 AVASKTYNLKKGQHTLEDFORVLDVNLMTGFNYIRLVAGEMQNEPDGQGRGVIINTA 154
    |||||
DB 61 AVASKTYNLKKGQHTLEDFORVLDVNLMTGFNYIRLVAGEMQNEPDGQGRGVIINTA 120
QY 155 SVAAFEQGVGAASASAKSGIVGNTLPARDLAPIGIRVMTIAPGLFTPLTSLPERKVC 214
    |||||
DB 121 SVAAFEQGVGAASASAKSGIVGNTLPARDLAPIGIRVMTIAPGLFTPLTSLPERKVC 180
QY 215 NFLASQVFPFSLGDPAEYAHVQAIIENPFLNGEVRILDGAIIRMP 261
    |||||
DB 181 NFLASQVFPFSLGDPAEYAHVQAIIENPFLNGEVRILDGAIIRMP 227
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RESULT 8
US-09-966-262-245
; Sequence 245, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
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;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,154
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/054,804
;; PRIOR FILING DATE: 1997-08-05
;; PRIOR APPLICATION NUMBER: US 60/056,370
;; PRIOR FILING DATE: 1997-08-19
;; PRIOR APPLICATION NUMBER: US 60/060,862
;; PRIOR FILING DATE: 1997-10-02
;; NUMBER OF SEQ ID NOS: 343
;; SOFTWARE: PatentIn ver. 2.0
;; SEQ ID NO 245
;; LENGTH: 227
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-966-262-245
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Query Match 87.1%; Score 1136; DB 9; Length 227;  
Best Local Similarity 99.6%; Pred. No. 3.2e-93;  
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 35 ASAYLLDLPNSGGGAQAKKLGNNVVFAPADVTSEKDVQTALALAKGFGYDVAVNCAGI 94
    |||||
DB 1 ASAYLLDLPNSGGGAQAKKLGNNVVFAPADVTSEKDVQTALALAKGFGYDVAVNCAGI 60
QY 95 AVASKTYNLKKGQHTLEDFORVLDVNLMTGFNYIRLVAGEMQNEPDGQGRGVIINTA 154
    |||||
DB 61 AVASKTYNLKKGQHTLEDFORVLDVNLMTGFNYIRLVAGEMQNEPDGQGRGVIINTA 120
QY 155 SVAAFEQGVGAASASAKSGIVGNTLPARDLAPIGIRVMTIAPGLFTPLTSLPERKVC 214
    |||||
DB 121 SVAAFEQGVGAASASAKSGIVGNTLPARDLAPIGIRVMTIAPGLFTPLTSLPERKVC 180
QY 215 NFLASQVFPFSLGDPAEYAHVQAIIENPFLNGEVRILDGAIIRMP 261
    |||||
DB 181 NFLASQVFPFSLGDPAEYAHVQAIIENPFLNGEVRILDGAIIRMP 227
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RESULT 9
US-09-963-966-245
; Sequence 245, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
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Thu Jun 26 06:55:09 2003

us-09-931-186-6.rapb

Page 4

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Db 61 AAPADVSEKVOYALALAKKRGVAVVAVNACAGIAVASTYNNKKQTHLEDFQVLYLV 120
Qy 121 NLMGTFVIRLVAGEMQNEPDGQGVLIINTASVAAREGVGAQAAVSASKGIYGMTL 180
Db 121 NLMGTFVIRLVAGEMQNEPDGQGVLIINTASVAAREGVGAQAAVSASKGIYGMTL 180
Qy 181 PIARDLAPIGIRVMTIPGIFGPELLLSPEKVCNLSASVPPPSLGDPAEYAHLYVQAI 240
Db 181 PIARDLAPIGIRVMTIPGIFGPELLLSPEKVCNLSASVPPPSLGDPAEYAHLYVQAI 240
Qy 241 IENPFLNGEYIRLDGAIKMQP 261
Db 241 IENPFLNGEYIRLDGAIKMQP 261
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RESULT 6

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US-09-931-186-2
; Sequence 2, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: AGREO, MELWYN A.
; APPLICANT: AGREO, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: RESTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPCZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length mutant ERAB C214R
US-09-931-186-2
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Query Match 98.7%; Score 1287; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 1.5e+106;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MAACRSYKGLAVITGASGLATAEIRLVGOGASAVLLDLPSNGSGPAQAKKIGNVVF 60
Db 1 MAACRSYKGLAVITGASGLATAEIRLVGOGASAVLLDLPSNGSGPAQAKKIGNVVF 60
Qy 61 APADVTSEKDVOTATLAKKRGKRVAVVAVNACAGIAVASTYNNKKQTHLEDFQVLYDV 120
Db 61 APADVTSEKDVOTATLAKKRGKRVAVVAVNACAGIAVASTYNNKKQTHLEDFQVLYDV 120
Qy 121 NLMGTFVIRLVAGEMQNEPDGQGVLIINTASVAAREGVGAQAAVSASKGIYGMTL 180
Db 121 NLMGTFVIRLVAGEMQNEPDGQGVLIINTASVAAREGVGAQAAVSASKGIYGMTL 180
Qy 181 PIARDLAPIGIRVMTIPGIFGPELLLSPEKVCNLSASVPPPSLGDPAEYAHLYVQAI 240
Db 181 PIARDLAPIGIRVMTIPGIFGPELLLSPEKVCNLSASVPPPSLGDPAEYAHLYVQAI 240
Qy 241 IENPFLNGEYIRLDGAIKMQP 261
Db 241 IENPFLNGEYIRLDGAIKMQP 261
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RESULT 7
US-09-984-245-245
; Sequence 245, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
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Query Match 87.1%; Score 1136; DB 9; Length 227;
US-09-984-245-245
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; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931.186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 20
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length mutant ERAB C214A
US-09-931-186-20

Query Match          98.8%; Score 1290; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 8.2e-107;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 61 APADVTSEKDVOTATLAKGKRGVDVAVNCAGIAVASKTYNKKGGTHLEDFORVLDV 120
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DB 121 NMGTFFVIRLVAGEMGNPEPDGGRGVINTASVAPEGQVGAAYSAKSGIYGMTL 180
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DB 181 PIARDLAPIGIRMTIAPGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEYIRLDGAIKMQP 261
DB 241 IENPFLNGEYIRLDGAIKMQP 261

RESULT 4
US-09-931-186-4
; Sequence 4, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, CHARLES S.
; APPLICANT: AGREST, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPCZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931.186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 261
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length mutant ERAB C5V
US-09-931-186-4

Query Match          98.8%; Score 1289; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 1e-106;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAACRSYKGLAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEQAQAKKLGNNVF 60
DB 1 MAAACRSYKGLAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEQAQAKKLGNNVF 60
QY 61 APADVTSEKDVOTATLAKGKRGVDVAVNCAGIAVASKTYNKKGGTHLEDFORVLDV 120
DB 61 APADVTSEKDVOTATLAKGKRGVDVAVNCAGIAVASKTYNKKGGTHLEDFORVLDV 120
QY 121 NMGTFFVIRLVAGEMGNPEPDGGRGVINTASVAPEGQVGAAYSAKSGIYGMTL 180
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QY 181 PIARDLAPIGIRMTIAPGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHVQAI 240
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QY 241 IENPFLNGEYIRLDGAIKMQP 261
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RESULT 5
US-09-931-186-23
; Sequence 23, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPCZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931.186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 23
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length mutant ERAB C214S
US-09-931-186-23

Query Match          98.8%; Score 1289; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 1e-106;
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93 233 17.9 311 9 US-09-738-626-3819 Sequence 3819, Ap  
94 231 17.7 261 10 US-09-815-242-5813 Sequence 5813, Ap  
95 225.5 17.3 247 10 US-09-815-242-11342 Sequence 11342, A  
96 224 17.2 254 10 US-09-741-669-411 Sequence 411, App  
97 223.5 17.1 900 9 US-10-060-230-15 Sequence 15, Appl  
98 223.5 17.1 900 9 US-10-060-230-17 Sequence 17, Appl  
99 222.5 17.1 247 10 US-09-815-242-11514 Sequence 11514, A  
100 217.5 16.7 233 10 US-09-815-242-10279 Sequence 10279, A

## ALIGNMENTS

## RESULT 1

US-09-931-186-6  
Sequence 6, Application US/09931186  
Patent No. US20020132319A1  
GENERAL INFORMATION:  
APPLICANT: ABREO, MELWYN A.  
APPLICANT: AGREE, CHARLES S.  
APPLICANT: AUST, ROBERT  
APPLICANT: KISSINGER, CHARLES R.  
APPLICANT: MARGOSIAR, STEVE  
APPLICANT: MENG, JERRY J.  
APPLICANT: PELLETIER, LAURA A.  
APPLICANT: REJTO, PAUL A.  
APPLICANT: SHOWALTER, RICHARD E.  
APPLICANT: TEMPCZYK-RUSSELL, ANNA  
APPLICANT: THOMSON, JIM  
APPLICANT: VANDERPOOL, DARIN  
APPLICANT: VILLAFRANCA, J. ERNEST  
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL  
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION  
FILE REFERENCE: 0125-0049  
CURRENT APPLICATION NUMBER: US/09/931,186  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 261  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: full length mutant ERAB C58V  
US-09-931-186-6

Query Match 100.0%; Score 1304; DB 10; Length 261;  
Best Local Similarity 100.0%; Pred. No. 4.7e-108;  
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DB 121 NLMGTNVIRLVAGEMQNEPDGQGGVYIINTASVAEFGVGOAAYSASKGIVGMTL 180  
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DB 181 PIARDLAPIGIRVMTIAPGLFGTPLTSLPEKYCNFLASQVPPSRIGDPAEYAHLYOAI 240  
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DB 241 IENPFLNGEYIRLDGAIRMOP 261

RESULT 2

US-09-931-186-8  
Sequence 8, Application US/09931186  
Patent No. US20020132319A1  
GENERAL INFORMATION:  
APPLICANT: ABREO, MELWYN A.  
APPLICANT: AGREE, CHARLES S.  
APPLICANT: AUST, ROBERT  
APPLICANT: KISSINGER, CHARLES R.  
APPLICANT: MARGOSIAR, STEVE  
APPLICANT: MENG, JERRY J.  
APPLICANT: PELLETIER, LAURA A.  
APPLICANT: REJTO, PAUL A.  
APPLICANT: SHOWALTER, RICHARD E.  
APPLICANT: TEMPCZYK-RUSSELL, ANNA  
APPLICANT: THOMSON, JIM  
APPLICANT: VANDERPOOL, DARIN  
APPLICANT: VILLAFRANCA, J. ERNEST  
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL  
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION  
FILE REFERENCE: 0125-0049  
CURRENT APPLICATION NUMBER: US/09/931,186  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 261  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: wild type ERAB  
US-09-931-186-8

Query Match 99.6%; Score 1299; DB 10; Length 261;  
Best Local Similarity 99.6%; Pred. No. 1.3e-107;  
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RESULT 3  
US-09-931-186-20  
Sequence 20, Application US/09931186  
Patent No. US20020132319A1  
GENERAL INFORMATION:  
APPLICANT: ABREO, MELWYN A.  
APPLICANT: AGREE, CHARLES S.  
APPLICANT: AUST, ROBERT  
APPLICANT: KISSINGER, CHARLES R.  
APPLICANT: MARGOSIAR, STEVE  
APPLICANT: MENG, JERRY J.  
APPLICANT: PELLETIER, LAURA A.  
APPLICANT: REJTO, PAUL A.  
APPLICANT: SHOWALTER, RICHARD E.  
APPLICANT: TEMPCZYK-RUSSELL, ANNA

Thu Jun 26 06:55:09 2003

us-09-931-186-6.rapb

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

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(without alignments)  
1388.950 Million cell updates/sec

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Perfect score: 1304  
Sequence: 1 MAACRSVKGLVAVITGAS.....ENPFLNGEYIRLDGAIKMP 261

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Searched: 417779 seqs, 108205813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database : Published Applications\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1289	98.9	261	10	US-09-931-186-20
4	1289	98.8	261	10	US-09-931-186-4
5	1289	98.8	261	10	US-09-931-186-23
6	1287	98.7	261	10	US-09-931-186-2
7	1136	87.1	227	9	US-09-984-245-245
8	1136	87.1	227	9	US-09-986-262-245
9	1136	87.1	227	9	US-09-983-966-245
10	1136	87.1	227	9	US-10-143-090-245
11	664.5	51.0	388	9	US-09-920-923-411
12	332.5	25.5	259	10	US-09-931-186-17
13	331.5	25.4	243	10	US-09-815-242-13360
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15	314	24.1	237	9	US-10-175-096-12
16	314	24.1	237	9	US-09-823-901-12
17	308.5	23.7	245	10	US-09-815-242-10921
18	305.5	23.4	253	10	US-09-931-186-15
19	301	23.1	247	9	US-09-479-040-9

20	297.5	22.8	267	9	US-09-773-748-1	Sequence 1, Appl1
21	292.5	22.4	262	10	US-10-307-385-6	Sequence 6, Appl1
22	292.5	22.4	262	10	US-09-802-883-6	Sequence 6, Appl1
23	290.5	22.3	270	9	US-09-978-295A-468	Sequence 468, App
24	290.5	22.3	270	9	US-09-978-697-468	Sequence 468, App
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26	290.5	22.3	270	9	US-09-999-832A-468	Sequence 468, App
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28	290.5	22.3	270	9	US-09-978-608A-468	Sequence 468, App
29	290.5	22.3	270	9	US-09-978-191A-468	Sequence 468, App
30	290.5	22.3	270	9	US-09-978-403A-468	Sequence 468, App
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33	290.5	22.3	270	9	US-10-017-081A-468	Sequence 468, App
34	290.5	22.3	270	9	US-09-981-915A-468	Sequence 468, App
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53	288.5	22.1	642	9	US-09-364-847-61	Sequence 61, Appl1
54	288.5	22.1	642	9	US-09-364-847-61	Sequence 61, Appl1
55	285.5	21.9	244	9	US-09-869-092-13	Sequence 13, Appl1
56	283.5	21.7	203	10	US-10-175-696-19	Sequence 19, Appl1
57	283.5	21.7	203	10	US-09-823-901-17	Sequence 7, Appl1
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59	276.5	21.2	254	9	US-09-978-758-2	Sequence 2, Appl1
60	276	21.2	258	9	US-09-738-626-6436	Sequence 6436, App
61	274	21.0	206	9	US-09-997-816-4	Sequence 4, Appl1
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72	266	20.4	285	10	US-09-815-242-10241	Sequence 10241, A
73	263	20.2	276	9	US-09-944-160-24	Sequence 24, Appl1
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83	249	19.1	221	10	US-09-764-553-553	Sequence 553, App
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86	242.5	18.6	274	9	US-09-976-059-17	Sequence 17, Appl1
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91	235	18.0	271	10	US-09-815-242-13387	Sequence 13387, A
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R;Tetelid, H.; Nelson, K.E.; Paulsen, I.T.; Eelsen, J.A.; Read, T.D.; Peterson, S.; Heid  
nson, J.D.; Omagari, L.A.; White, O.; Salzbarg, S.L.; Lewis, M.R.; Radune, D.; Holtapple,  
nson, T.; Hickley, E.R.; Holt, I.E.  
Science 293, 498-506, 2001

A:Authors: lotius, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: G95048

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 17243 <KUR>

A:Cross-references: GB:AEO05672; PIDN:AAK74584.1; PID:g1q1971891; GSPEB:GN00164; TIGR:SP4

C:Genetics:

C:Experimental source: strain TIGR4

C:Gene: SP0421

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Db 6 LLEKVALVVGASGSGIKAIETLAEAGAKVIGTATSESGAOAASDYLGDGKGMALNVT 65

QY 67 SENVOYQALALAKKFEGRVYAVNCAGIAVASKTYNLKGGTHTLDEFOYRLVYNLMGTF 126

Db 66 NPSIEIYVLAKITDEFGVDLVNNAGITRDNLMPKKE-----EESDMEITNLSTIF 119

QY 127 NVIRLVAGEMQNPEDGGGORGVIINTASVAAFEGVQQAAYSASKSGIVGMLPIARDL 186

Db 120 RLKSAVLRGMAKK-----RGRITINGVSVGTGNGNQAANYAAAKAGVIGFTKSMAREV 173

QY 187 APIGRWITAPGLFGTLPILSLPEKCNFLASQVPPSRUTRGADEVAHLVQATLEND-- 244

Db 174 ASRGVYNTVAPGIEIDMTKALNDEQRTATLAQVP-AGRLGDPREIASAV-ATLASPEA 231

QY 245 -FLNGEVIRLDGAIRM 259

Db 232 AVITGETLVHVGGMYM 247

RESULT 21

H86721 hypothetical protein fabd1 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001

C:Accession: F86721

R:Bojoltin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarum, K.; Weissenbach, J.; Ehrigmeier, N.; 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis strain IL1403

A:Reference: A86625; MUID:21235186; PMID:11337471

A:Accession: F86721

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-243 <STD>

A:Cross-references: GB:AA005176; PID:G12736993; PIDN:AAK04872.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: fabd1

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.9%; Score 324.5; DB 2; Length 243;

Best Local Similarity 31.7%; Pred. No. 1.le-17;

Matches 82; Conservative 48; Mismatches 104; Indels 25; Gaps 6;

QY 8 VKGLAVVITVGASGSLTAETALVVGQASAVLLDLPNGSGEAOAKLT-----GNNVVF 60

Db 3 IKNNVFEVITGSTRGKRALQPAKAGSNLII-----NGRAISBELLAETAVGAVAG 57

QY 61 APADVTSEKDVOTALALAKKFEGRVDAVNCAGIAVASKTYNLKGGTHTLDEFOYRLVDV 120

Db 58 ISGDISKEDAKOMAEALIEITLGSVDILVNNAGI--TRDGLSLKMSR---EDGESVTKI 111

QY 121 NLMGFNFIIRLVAGEMQNEPDGORGVIINTASVAAFEGVQQAAYSASKSGIVGMLT 180

Db 112 NLTGFMNTQAVL-----KMTARSAIINISSVVGMLKMNQAQANAAAKAGLIGITK 165

QY 181 PIARDLAPIGIRVMTIAPGLFGTLPILSLPKVCNFLASQVPPSRUGDPREIYHLVQAT 240

Db 166 SIARVAVARNRVAVNAAGFIESDTEVLSKVYDAMKGIIPM-KRFGMPPEIATATQEL 224

QY 241 IENPENGVIRLDGAIRM 259

Db 225 ADEQVMTQGVLTIDGCVSM 243

RESULT 22

T36846 probable dehydrogenase - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 11-Jan-2000

C:Accession: T36846

R:Oliver, K.; Harris, D.; Parkhill, J.; Bartell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, September 1998

A:Reference number: Z21615



C:Accession: S22450; S19832  
R:Klein, B.; Pawlowski, K.; Hoerlicke-Grandpierre, C.; Schell, J.; Toeplitz, R.  
Mol. Gen. Genet. 233: 122-128, 1992  
A:Title: Isolation and characterization of a cDNA from *Cuphea lanceolata* encoding a beta  
A:Reference number: S22450; MUID:92293104; PMID:1376402  
A:Accession: S22450  
A:Molecule type: mRNA  
A:Residues: 1-320 <KLE>  
A:Cross-references: EXBL:W64566; NID:G18045; PIDN:CAA45866.1; PID:G18046  
A:Experimental source: Immature embryo  
C:Genetics:  
A:Gene: CLKr27  
A:Genome: nuclear  
C:Function:  
A:Description: EC 1.1.1.100 [validated, MUID:92293104]  
A:Pathway: fatty acid biosynthesis  
A>Note: Integral part of the fatty acid synthase type II  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
C:Keywords: chloroplast; fatty acid biosynthesis; NADP; oxidoreductase  
F:1-63/Domain: transit peptide (chloroplast) #status predicted <NP>  
F:64-320/Product: 3-oxoacyl-[acyl-carrier-protein] reductase #status predicted <NAT>  
F:78-258/Domain: short-chain alcohol dehydrogenase homology <SADP>  
F:127/Active site: Tyr #status predicted

[illegible]

RESULT 17  
C83961  
3-oxoacyl-(acyl-carrier protein) reductase fabg [imported] - *Bacillus halodurans* (strain C:Species: *Bacillus halodurans*  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 03-Aug-2001  
C:Accession: C83961  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirata  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
A:Reference number: AB6560; MUID:20512582; PMID:11058132.  
A:Accession: C83961  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-246 <STD>  
A:Cross-references: GB:AB001515; GB:BA000004; NID:g10174886; PIDN:BA06210.1; GSPDB:GN000  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: fabg  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

QY 8 KKGIVAITGASLSGLATSERLYGOGASAVLDDLPSSGE-----AQARKLGNVV 59  
 Db 2 LGGTALATYGTASRIGGATMELARHGANVV-----NYAKKEKAERVVAIEKELSYEAI 57  
 QY 60 FAPADVTSEKDVCTALALANGKFGVADVAVNACIGIAVASTYNNKKQCHTLEDFQVLD 119  
 Db 58 AICQADVADSESVQAMVEXETIDTFEGAVDILVNNAGITDNNFMRYKE-----EDMDAYID 111  
 QY 120 VNLGTFENVITLVAGEKQNEPDQGGOR-GVIINTASVAALPEQGVGOAAVSASKGIIVGM 178  
 Db 112 TNLGVGHRCSAAVTRPMK-----QRFGLIIVSSYVCAIGNAGQANYYAAAGVIGL 164  
 QY 179 TLPIARDIAPIGIVNMTIAPGLFETPLLTSLPEKVCNPLASQVFPSPRLQDPATYAHLVQ 238  
 Db 165 TKTLARELIANNITVNNVAVAPGFIETDMTGELPEDEVKQOMQOPL-ARLQPREVAKAVR 223  
 QY 239 AIIEEN--PFLNGEVIRLDGAIRM 259  
 Db 224 FLASDDASLYLQGTIIHNGKVM 246

RESULT 18  
E97919  
3-xoxacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [Imported] - Streptococcus  
C.Species: Streptococcus pneumoniae  
C.Date: 22-oct-2001 #sequence\_revision 22-Oct-2001 #text\_charge 02-Nov-2001  
C.Accession: E97919  
R.Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; DeHoff, B.S.  
E. K.; LeBlanc, D.J.; Lee, L.N.; LeFKowitz, E.C.; Lu, J.; Matsushima, F.; McAhren, S.  
Y. P.; Sun, P.W.; Winkler, M.E.  
J. Bacteriol., 183, 5709-5717, 2001  
A.Author: Yang, Y.; Young-Bellid, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.  
A.Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A.Reference number: A97872; MUID:21429245; PMID:11544234  
A.Accession: E97919  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-243 <KOR>  
A.Cross-references: GB:AE007317; PIDD:AAK99185.1; PID:g15457942; GSPDB:GN00174  
C.Genetics:  
A.Gene: xabB  
A.Gene\_family: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
C.Keywords: oxidoreductase

Query Match	25.4%;	Score	331.5;	DB	2;	Length	243;
Best Local Similarity	35.5%;	Pred.	No. 3,1e-18;				
Matches	89;	Conservative	36;	Mismatches	103;	Indels	23;
				Gaps	6;		

  

QY	15	ITGASGSLGTAETARLWVGASAVLLDLPNSGGE----	AQAKKITGNVVFAPADVTEE	68
		:       :     :     :	:     :	
Db	10	ITGSSRSGIGLAIARKEFAQAGANIYV----	NSRGAISELLAEFSNNGIKVPIPSGDVSP	65
		:       :     :     :	:     :	
QY	69	KDVQTALALAGKRGKRDVAANCNGIIVASKTYLKKGGHTLEDORVLVDVLMGTFFV	128	
		:       :     :     :	:     :	
Db	66	ADARMRIDQALAEIGSVDLVNNAGI--TQDTMLKY----	TEADFEKVKLVKLVTGAFFNK	119
		:       :     :     :	:     :	
QY	129	IRLVAGEKGONEDPOGGQGVIIINTASVAAFEGOVGCAASASKGGIVGKTLPIARDLP	188	
		:       :     :     :	:     :	
Db	120	TQSVL-----KPMKAKREGALIMSSVVGIMNGIGCANVAASAGLIGFTKSVAREVAS	173	
		:       :     :     :	:     :	
QY	189	IGIRVMTIAPLEFCTPLITSLPEKVCNCFLASQVFPFRLDDPAEYIAHLVQAIITENPLNG	248	
		:       :     :     :	:     :	
Db	174	RNIRRNVAIVPMISMDSMTAILSDRIKEATLQAIIPM-KEFGAEEQVADILVFELAGODYLTG	232	
		:       :     :     :	:     :	
QY	249	EVIRLDGAIRM	259	
		:       :     :     :	:     :	
Db	233	QYTAIDGGLSM	243	

  

RESULT	19
GS048	
3-oxoacyl-[acyl-carrier protein] reductase [imported] - Streptococcus pneumoniae (str	
C:Species: Streptococcus pneumoniae	



## RESULT 10

F83098  
Probable short-chain dehydrogenase PA4389 [imported] - Pseudomonas aeruginosa (strain PA  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: F83098  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: F83098  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1,252 <STO>  
A:Cross-references: GB:AE004854; GB:AE004091; NID:99950606; PIDN:AA07777.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA4389  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 27.2%; Score 355; DB 2; Length 252;  
Best Local Similarity 35.1%; Pred. No. 5,1e-20;

Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;

QY 8 VKGLVAVITGGASGLGATAEFLVYOGASAVILDPN-----SGEQAQAKKG 55  
DB 3 LKDRVITITGGCCGGLGAKGEVLAGKARLALVDLNERLDEAVACKAGGARA--- 58  
QY 56 NNVFAPADVTSEKDVOTALAKKRGYDVAVNCAGIAVASTYVNLKQGTHT--TLED 113  
DB 59 -----YVCNVADEQVTHVMAOVAVSDFGALNGLVNNGNLRDGTITVKKQGSLSLAQ 113  
QY 114 FQRLVDVNLKGTENVITRLVAGEMQ--NEPDQGGQGVITINTASVAEFEGVQAASVS 171  
DB 114 WQSVIDVNLGVFLCTEVEVAKMELNE-----GAIYNTSSISR-AGNMQOANSAA 165  
QY 172 KGTIVGMTLPFARLDPIGIRVMTIADGFTGTPPLTSLPKVCNFIASQVPPSRLGDP 231  
DB 166 KAGVAADTVWAKKLAVGIRVAGVAPGFIETEMTACMKPEALEKMTAGIPL-KRMGRV 224  
QY 232 EYAHVQAIIENPFLNGEVIRLDGAIRM 259  
DB 225 EIAHSVAVYIFENDYYTGTGVLLELDGRL 252

## RESULT 11

H72219  
3-oxoacyl-(acyl carrier protein) reductase - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: H72219

R:Neelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.  
C.M.

Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: H72219

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1,246 <ARN>

A:Cross-references: GB:AE001811; GB:AE000512; NID:94982291; PIDN:AAJ36790.1; PID:9498230  
A:Experimental source: strain MSB8  
C:Genetics:

A:Gene: TM1724  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

F:6-185/Domain: short-chain alcohol dehydrogenase homology <SAD>

Query Match 26.5%; Score 346; DB 2; Length 246;

Best Local Similarity 34.1%; Pred. No. 2,4e-19;  
Matches 87; Conservative 47; Mismatches 103; Indels 18; Gaps 5;

QY 8 VKGLVAVITGGASGLGATAEFLVYOGASAVILDPNNGGGA---QAARKNNVFAPAD 64  
DB 3 LEGKCVLITIGASAGSKNTTLTLLFAEGATVLAGDSKENDLSIVAEAGLGKQDPVYLN 62  
QY 65 VTSEKDVOTALAKKRGYDVAVNCAGIAVASTYVNLKQGTHTLEDFOVRLDYNLMG 124  
DB 63 VYDRQIKKVEKRYVOKYGRDYLAVNNAGITREDALLVRKE-----EDMDAVIVNVLKG 116  
QY 125 TFNVITRLVAGEGONEDPDQGGQGVITINTASVAEFEGVQAASKSGIAGMTLPAR 184  
DB 117 VENVITQVYPMIKO-----RNGSIVAVSSVYIGNPGQNTNAAASKAGVIGMTKTMK 170  
QY 185 DLAPIGIRVMTIAPGLFTGTPPLTSLPKVCNFIASQVPPSRLGDPAEYAHLY--QAITE 242  
DB 171 ELAGRIRIVNAVAPGFIETPMTKEKPEKARETALSRIPL-GRFGKPEEVAQVILFLASDE 229  
QY 243 NFPLNGEVIRLDGAIR 257  
DB 230 STVITGQVIGIDGGL 244

## RESULT 12

F97338  
3-ketocyl-acyl carrier protein reductase [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: F97338

R:Kolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: F97338  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1,249 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK81497.1; PID:915026670; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:

A:Gene: CAC3574  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.3%; Score 343.5; DB 2; Length 249;  
Best Local Similarity 33.2%; Pred. No. 3,9e-19;

Matches 86; Conservative 56; Mismatches 96; Indels 21; Gaps 6;

QY 8 VKGLVAVITGGASGLGATAEFLVYOGASAVILDPNNGGGA---AKKGNVVFAP 62  
DB 5 LSGKVAVITGGAGGLRALNLKLAAGANLY-VNYSSEAFQKLIKELBELGSKAVAYK 63  
QY 63 ADVTSEKDVOTALAKKRGYDVAVNCAGIAVASTYVNLKQGTHTLEDFOVRLDYNL 122  
DB 64 ADTSKDEMETIKKALDEGVYDLYVNNAGITKMDLLFMKE-----EDPDSVYNVL 117  
QY 123 MGFENVITRLVAGEGONEDPDQGGQGVITINTASVAEFEGVQAASKSGIAGMTLP 182  
DB 118 KGFAPNCKHTRSYMLK-----KSKITNISSVIGLIGNAGOVNAAAKAGIIGTKSV 171  
QY 183 ARDLAPIGIRVMTIAPGLFTGTPPLTSLPKVCNFIASQVPPSRLGDPAEYAHLY 242  
DB 172 AKELASRGITVNAVAGIISDWTALTDKQRESIVAAYPL-NKVGAEADVAVNLVFLAS 230  
QY 243 --NFPLNGEVIRLDGAIRM 259  
DB 231 DLSYITGCVINVDGGMV 249

## RESULT 13

T51084  
3-oxoacyl-(acyl carrier protein)-reductase (oar-1) [imported] - Neurospora crassa

Db 238 NDYMGVIRLDGAIKMP 256

# RESULT 7

AG2750

3-hydroxyacyl-CoA dehydrogenase type II Atul415 [imported] - Agrobacterium tumefaciens C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002

C:Accession: AG2750

R:Wood, D.W.; Seubald, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kulyavin, I.; Levy, R.; Li, M.; McClellan, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AG2750

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-257 <KUR>

A:Cross-references: GB:AE00688; PIDN:AL42421.1; PID:q17739833; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atul415

A:Map position: circular chromosome

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 49.2%; Score 642; DB 2; Length 257;

Best Local Similarity 51.7%; Pred. No. 5.2e-42;

Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

Db 7 SVKGVAVITGASGLIATERYVGQASAVLLDPSNGEQAOKLGNVYFAPADY 66

2 NIEGAGALVTGAAGLGAARMAARAAATITDRNGEKKLAIEIGRAV--GGDVT 59

67 SEKDQVTLALAKGFGVDVAVNCAGIAVASKTYNKKGGTHTLEFORLYDVNLMTGE 126

60 SDADQAAIKVAASKSGRLRLVNCAGIGTAGRI--LGRREPQLGSEFGYIRNLTGTF 117

127 NVIRLVAGEMGQNEPDG----GGRVITNTASVAATFEGVQAAYSASKGGIYGMPLT 182

118 NMRLAAAHMAEREDGSDRQDNGVTVNTASVAATFEGVQAAYSASKGGIYSLALPA 177

183 ARDLAPIGIRVMTAPGLFGFTPLTSLPEKVCNPLASQVPPSRGLGPAEYAHVQAITE 242

178 ARELARFRIRVNTYAPGIFLPLIQLGFPQVQESLQGIPIHPSRLGDPAEFADIVRELT 237

243 NFPLNGEVIRLDGAIKMP 261

238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

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Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

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Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

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Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Db 238 NDYMGVIRLDGAIKMP 256

Query Match 45.6%; Score 595; DB 2; Length 260;

Best Local Similarity 51.0%; Pred. No. 2.1e-38;

Matches 130; Conservative 30; Mismatches 89; Indels 6; Gaps 2;

Db 11 LVAVITGASGLIATERYVGQASAVLLDPSNGEQAOKLGNVYFAPADY 70

7 VAAVITGASGLIATERYVGQASAVLLDPSNGEQAOKLGNVYFAPADY 64

71 VQTALALAKGFGVDVAVNCAGIAVASKTYNKKGGTHTLEFORLYDVNLMTGE 126

65 VAGEKRAAAGQERILVNCAGIGTAGRI--LGRREPQLGSEFGYIRNLTGTF 124

127 NVIRLVAGEMGQNEPDGQGRVITNTASVAATFEGVQAAYSASKGGIYGMPLT 186

125 KCIASAKGMLDLEPLEDGERGAIYNTASVAATFEGVQAAYSASKGGIYGMPLT 184

187 APGIRVMTAPGLFGFTPLTSLPEKVCNPLASQVPPSRGLGPAEYAHVQAITE 246

185 MGEIRVMTAPGLFGFTPLTSLPEKVCNPLASQVPPSRGLGPAEYAHVQAITE 244

247 NGEVIRLDGAIKMP 261

245 NGEVIRLDGAIKMP 259

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

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Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Db 247 NGEVIRLDGAIKMP 261

Probable [jpmo03] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA  
C:Species: Sinorhizobium meliloti  
C>Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C:Accession: H95360

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bower,  
J.; Kallman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Strzycki, R.; Wells, D.H.; Yeh, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A>Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: H95360

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 <GR>

A:Cross-references: GB:AE006469; PIDN:AAK65450.1; PID:G14523918; GSEDB:GN00165

A:Experimental source: strain 1021, megaplasmid pSymA

A:Expilbert, F.; Flann, T.M.; Long, S.R.; Punher, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.,  
L.: Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kallman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
heault, P.; Vandenhof, M.; Vorholter, F.; J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.

A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

C:Contents: annotation

C:Genetics:

A:Gene: Smal452

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Genetics:  
A:Gene: RV1144  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
F:6-187/Domain: short-chain alcohol dehydrogenase homology <SAD>

Query Match 51.5%, Score 671.5; DB 2; Length 250;  
Best Local Similarity 60.1%; Pred. No. 2.8e-44;  
Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;

QY 9 KGLVAVITGGASGIGLATAERLVGQASAVLLDLPNSGGEAQAKKGNVVFAPADVTSE 68  
| | | | | : | | | | | : | | | | | : | | | | |  
Db 4 KDAAVAAYTGGSSGIGLATRKRLLDAGQAVYYVD---RGDDVYGCLDDRFAQADVTDE 60  
| | | | | : | | | | | : | | | | | : | | | | |

QY 69 KDVOATALAKGRFGRVDAVNCAGIAVASKTIVLKKGQHTLEDFORYLDVNLMGFNV 128  
| | | | | : | | | | | : | | | | | : | | | | |  
Db 61 AAVSAALELA-DSLGPVAVVVNVCAGTGNAIRV--LSRDGVFPPLAFRIYDINVGTFNV 117  
| | | | | : | | | | | : | | | | | : | | | | |

QY 129 IRIVAGEGMONEPPOGGRGVIINTASTAAFEQGVGOGAASGKIYGMTPIARDLAP 188  
| | | | | : | | | | | : | | | | | : | | | | |  
Db 118 LRLGAERLAKKEP-IGEBRGVIINTASTAAPDGIQAAYASASGVGMPLIARDLAS 176  
| | | | | : | | | | | : | | | | | : | | | | |

QY 189 IGRIVMTAPGIFGTPLITSPEKYCNFLASQVPSPSLGDPABAYHLVQAIINPLNG 248  
| | | | | : | | | | | : | | | | | : | | | | |  
Db 177 KLIRVYTAPGIFPTPLIASLPAEKASKLGQOVPHPSLTGNPDXYGALVTHLIENPMNG 236  
| | | | | : | | | | | : | | | | | : | | | | |

QY 249 EYIRLDGAIKMP 261  
| | | | | : | | | | | : | | | | | : | | | | |  
Db 237 EYIRLDGAIKMAP 249  
| | | | | : | | | | | : | | | | | : | | | | |

RESULT 6  
F97531  
probable short-chain dehydrogenase (Pa254) [Imported] - Agrobacterium tumefaciens (S)  
C:Species: Agrobacterium tumefaciens  
C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
C:Accession: F97531  
R:Goodner, B.; Hinkle, G.; Gitting, S.; Miller, N.; Blanchard, M.; Ourullo, B.; Goldm  
A.; Liu, F.; Molim, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz,  
Science 294, 2333-2338, 2001  
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium  
A:Reference number: A97359; PMID:11743194  
A:Accession: F97531  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-257 <KUR>  
A:Cross-references: GB:AEO07869; PIDN:AAK87207.1; PJD:g15156487; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR\_C\_2613  
A:Map position: Circular chromosome  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 49.2%; Score 642; DB 2; Length 257;  
Best Local Similarity 51.7%; Pred. No. 5.2e-42;  
Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

QY 7 SVKGLAVITGGASGIGLATAERLVGQASAVLLDLPNSGGEAQAKKGNVVFAPADVT 66  
| | | | | : | | | | | : | | | | | : | | | | |  
Db 2 NIEGAGALTGGAASGIGAARMLARGAAVTIIPRNSEGAKKLAEIGKAV--QGDT 59  
| | | | | : | | | | | : | | | | | : | | | | |

QY 67 SEKDQOTALAKGRFGRVDAVNCAGIAVASKTYNLKKQTHTLEDFORYLDVNLMKGT 126  
| | | | | : | | | | | : | | | | | : | | | | |  
Db 60 SDADQAQAKVAASAKGGRILYNCAIGISTARI--LGRSGPQLDGDFQYIRVNLIGTF 117  
| | | | | : | | | | | : | | | | | : | | | | |

QY 127 NVIRLVAGEMONEPDC---GQRGVIINTASTAAFEQGVGOGAAYASASGIVGMTPI 182  
| | | | | : | | | | | : | | | | | : | | | | |  
Db 118 NMNRATAAMAREDEGDGDSQDNQGVYINTASTAAFEQIQIAAAYASASGIVSTLAPA 177  
| | | | | : | | | | | : | | | | | : | | | | |

QY 183 ARDLAPIGIRVMTIAPGLEGTPLITSPEKYCNFLASQVPSPSLGDPABAYHLVQALTE 242  
| | | | | : | | | | | : | | | | | : | | | | |  
Db 178 ABELAFRRIRVMTAPGIFLTPLOGIDPQVEESLAGQIPHPSRLGDPDEFADVTRPLE 237  
| | | | | : | | | | | : | | | | | : | | | | |

QY 243 NPFLNGEYIRLDGAIKMP 261  
| | | | | : | | | | | : | | | | | : | | | | |

## ALIGNMENTS

## RESULT 1

T20484

hypothetical protein F01G4.2 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C&gt;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000

C:Accession: T20484

R:Harris, B.

submitted to the EMBL Data Library, January 1996

A:Reference number: Z19281

A:Accession: T20484

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-258 &lt;WILD&gt;

A:Cross-References: EMBL:Z68341; PIDN:CAA92764.1; GSPDB:GN00022; CESP:F01G4.2

A:Experimental source: clone F01G4

C:Genetics:

A:Gene: CESP:F01G4.2

A:Map position: 4

A:Intons: 8/3; 116/3; 162/3; 209/3

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 57.4%; Score 748; DB 2; Length 258;

Best Local Similarity 59.9%; Pred. No. 3.9e-50;

Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;

QY 3 AACRSYKGVAVTTGGASGLGATAEKLVGOGASAVLDPNSGGEPAOKKLGNNVFPADVT 62

DB 2 SALRSTKGLVALVTGASGLGCAFAFLAKAGQVAIIDLPSKSGADVAKEITG--ITFP 59

QY 63 ADVTSEKDVQALALAKKFGKRVDAVAVNCAGIYAVSKTYNKKGOTHTLEDFORVLDVNL 122

DB 60 ASYTSSEEVAAFAKQVQAEVGRDLALVNCAGIYAFKLTYSVCKKHVDFEKKIRQITDVAV 119

QY 123 MGFNTYIRLVAGMGONPEPDGSGRGVITNTASVAEFEGOVGAAYASAKSGIGVGTLP 182

DB 120 LGFTNYIRHGVALMGHEHDANGORGVINTASVAFFDQTOGOSAYSASKGALVGMTLPL 179

QY 183 ARDLADIGIRVMTIAGLFTPLTSLPEKVCNFTLASQVFPSPRLGDPAEVAHLVQALTE 242

DB 180 ARDFAGGIRFNTIAGLMDTGPLLSLPEKVSFLAQLIPNSRLGHPHEGALVQAHTE 239

QY 243 NPLNGEVIRLDGAIKM 259

DB 240 NOYLNGETIRFDGALRM 256

## RESULT 2

H83326

Probable short-chain dehydrogenase PA2554 [imported] - *Pseudomonas aeruginosa* (strain PC:Species: *Pseudomonas aeruginosa*

C&gt;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: H83326

R:Stover, C.K.; Pham, X.Q.; Ewlin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam,

N.; Lory, S.; Olson, M.V.

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: A82950; MUID:20457337; PMID:10984043

A:Accession: H83326

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 &lt;STO&gt;

A:Cross-References: GB:AE004683; GB:AE004091; NID:g99448607; PIDN:AA05942.1; GSPDB:GN001

C:Genetics:

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 54.5%; Score 711; DB 2; Length 255;

Best Local Similarity 57.1%; Pred. No. 2.7e-47;

Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

QY 8 VKGLVAVTTGGASGLGATAEKLVGOGASAVLDPNSGGEPAOKKLGNNVFPADVT 67

DB 3 IENRFTLTGGSSGLGATAEKLVGOGASAVLDPNSGGEPAOKKLGNNVFPADVT 62

QY 68 EKDVTALALAKKFGKRVDAVAVNCAGIYAVSKTYNKKGOTHTLEDFORVLDVNLGTFN 127

DB 63 DTDGFAAATAAEAFSRIDVAVNCAGIYAFKLTYSVCKKHVDFEKKIRQITDVAV 120

QY 128 VIRLVAGMGONPEPDGSGRGVITNTASVAEFEGOVGAAYASAKSGIGVGTLP 187

DB 121 MLRLAEMAMNNEPQSGRGVITNTASVAEFEGOVGAAYASAKSGIGVGTLP 180

QY 188 PIGIRVMTIAGLFTPLTSLPEKVCNFTLASQVFPSPRLGDPAEVAHLVQALTEPFLN 247

DB 181 RFGIRVMTIAGLFTPLTSLPEKVCNFTLASQVFPSPRLGDPAEVAHLVQALTEPFLN 240

QY 248 GEVIRLDGAIKM 259

DB 241 GEVIRLDGAIKM 252

Query Match 54.5%; Score 711; DB 2; Length 255;

Best Local Similarity 57.1%; Pred. No. 2.7e-47;

Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

QY 8 VKGLVAVTTGGASGLGATAEKLVGOGASAVLDPNSGGEPAOKKLGNNVFPADVT 67

DB 3 IENRFTLTGGSSGLGATAEKLVGOGASAVLDPNSGGEPAOKKLGNNVFPADVT 62

QY 68 EKDVTALALAKKFGKRVDAVAVNCAGIYAVSKTYNKKGOTHTLEDFORVLDVNLGTFN 127

DB 63 DTDGFAAATAAEAFSRIDVAVNCAGIYAFKLTYSVCKKHVDFEKKIRQITDVAV 120

QY 128 VIRLVAGMGONPEPDGSGRGVITNTASVAEFEGOVGAAYASAKSGIGVGTLP 187

DB 121 MLRLAEMAMNNEPQSGRGVITNTASVAEFEGOVGAAYASAKSGIGVGTLP 180

QY 188 PIGIRVMTIAGLFTPLTSLPEKVCNFTLASQVFPSPRLGDPAEVAHLVQALTEPFLN 247

DB 181 RFGIRVMTIAGLFTPLTSLPEKVCNFTLASQVFPSPRLGDPAEVAHLVQALTEPFLN 240

QY 248 GEVIRLDGAIKM 259

DB 241 GEVIRLDGAIKM 252

## RESULT 4

H95360

Thu Jun 26 06:55:10 2003

us-09-931-186-6.rpr

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:23:47 ; Search time 15.6667 Seconds

(Without alignments)  
1601.559 Million cell updates/sec

Title: US-09-931-186-6

Perfect score: 1304

Sequence: 1 MAACRSVKGLVAVITGAS.....ENPFNGEVIILDGAIKMP 261

Scoring table: BLOSUM62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR.73.\*

1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the total being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	748	57.4	258	T20484	hypothetical prote
2	720	55.2	255	H83326	probable short-cha
3	711	54.5	255	AG361	3-oxoacyl-(acyl-ca
4	675	51.8	255	H95360	Probable [imported
5	671.5	51.5	250	A70554	Probable dehydroge
6	642	49.2	257	F97531	probable short-cha
7	642	49.2	257	AG2750	3-hydroxyacyl-CoA
8	595	45.6	260	C87264	3-hydroxyacyl-CoA
9	383.5	29.4	247	E70740	probable fabG2 pro
10	355	27.2	252	F83098	Probable short-cha
11	346	26.5	246	H72219	3-oxoacyl-(acyl ca
12	340.5	26.1	297	F751084	3-oxoacyl-(acyl-ca
13	335	25.7	246	H84136	3-oxoacyl-(acyl-ca
14	334.5	25.7	251	AH2042	3-oxoacyl-(acyl-ca
15	334	25.6	320	S22450	3-oxoacyl-(acyl-ca
16	333.5	25.4	246	C83961	3-oxoacyl-(acyl-ca
17	331.5	25.4	243	E97919	3-oxoacyl-(acyl-ca
18	330.5	25.3	243	G95048	3-oxoacyl-(acyl-ca
19	328.5	25.2	248	F82128	3-oxoacyl-(acyl-ca
20	324.5	24.9	260	F86721	hypothetical prote
21	324.5	24.9	259	T36846	Probable dehydroge
22	316.5	24.3	259	H98137	3-oxoacyl-(acyl-ca
23	316.5	24.3	296	E87260	3-oxoacyl-(acyl-ca
24	316.5	24.2	299	D90481	hypothetical prote
25	313.5	24.0	247	S77280	3-oxoacyl-(acyl-ca
26	313.5	24.0	260	A48154	short-chain alcoh
27	313	24.0	247	F82776	3-oxoacyl-(acyl re

30	312.5	24.0	240	2	H75014	3-oxoacyl-(acyl-ca
31	311	23.8	262	2	AB3545	toluenesulfonate z
32	310	23.8	249	2	AG3121	dehydrogenase Atu4
33	310	23.8	253	2	H98165	3-oxoacyl-(acyl-ca
34	309.5	23.7	267	2	T11579	probable short cha
35	309.5	23.7	244	2	AB0195	3-oxoacyl-(acyl-ca
36	309.5	23.7	246	2	A69621	3-oxoacyl-(acyl-ca
37	308.5	23.5	247	2	AG1300	3-ketoacyl-acyl ca
38	306.5	23.5	247	2	AG1672	3-ketoacyl-acyl ca
39	306	23.5	256	2	AT0406	probable dehydroge
40	305	23.4	250	1	S47054	probable dehydroge
41	305	23.4	260	2	H70758	probable fabG3 pro
42	303	23.2	248	2	H98258	3-oxoacyl-(acyl-ca
43	303	23.2	248	2	AI3025	3-oxoacyl-(acyl-ca
44	301	23.1	255	1	S39737	glucose 1-dehydrog
45	300.5	23.0	296	2	T26723	hypothetical prote
46	300	23.0	245	2	AE3517	3-oxoacyl-(acyl ca
47	300	23.0	255	2	B90495	hypothetical prote
48	299	22.9	252	1	S10707	20beta-hydroxyster
49	296.5	22.7	258	2	C70885	probable dehydroge
50	294	22.5	255	2	H84288	3-oxoacyl-(acyl-ca
51	294	22.5	265	2	T36396	probable short cha
52	293	22.5	249	1	B37762	bile acid 7-dehydr
53	292.5	22.4	303	2	T46064	short-chain alcoh
54	291.5	22.4	244	2	T14051	3-oxoacyl-(acyl-ca
55	291.5	22.4	248	2	H70447	3-oxoacyl-(acyl-ca
56	290	22.2	258	2	D95284	probable [imported
57	290	22.2	272	2	AG3359	glucose 1-dehydrog
58	289.5	22.2	244	1	B42147	3-oxoacyl-(acyl-ca
59	289.5	22.2	256	2	E72427	oxidoreductase, sh
60	288.5	22.1	246	1	RDALAE	acetoacetyl-CoA re
61	286.5	22.0	244	2	G90812	3-oxoacyl-[acyl-ca
62	286.5	22.0	244	2	C85672	3-oxoacyl-(acyl-ca
63	285.5	21.9	254	2	G75333	3-oxoacyl-acyl car
64	285	21.9	255	2	G82644	2,5-dichloro-2,5-c
65	284.5	21.8	248	2	E81695	3-oxoacyl-(acyl ca
66	284.5	21.8	257	2	A72395	oxidoreductase, sh
67	284	21.8	240	2	F87312	acetoacetyl-CoA re
68	283.5	21.7	244	2	AD0642	3-oxoacyl-[acyl-ca
69	282.5	21.7	246	1	DEKONG	acetoacetyl-CoA re
70	282.5	21.7	253	2	B86737	acetoaldehyde dehydrogen
71	282.5	21.7	272	2	A99950	hypothetical prote
72	282.5	21.7	251	2	C87474	hypothetical prote
73	282	21.6	255	2	D72377	oxidoreductase, sh
74	282	21.6	260	2	F82954	probable short-cha
75	279.5	21.4	241	1	S06998	acetoacetyl-CoA re
76	279	21.4	246	1	S28279	acetoacetyl-CoA re
77	279	21.4	258	2	B89773	acetoaldehyde dehydrogen
78	278	21.3	263	2	AB0812	probable oxidoredu
79	277	21.2	249	1	A31841	bile acid dehydrox
80	277	21.2	262	2	B97588	oxidoreductase, sh
81	277	21.2	262	2	AG2809	short chain dehydr
82	276.5	21.2	248	2	T44361	acetoacetyl-CoA re
83	275.5	21.1	248	2	F71538	probable oxoacyl (
84	275	21.1	267	2	B87578	hypothetical prote
85	274.5	21.1	248	2	B97223	probable 3-ketoacy
86	274	21.0	259	2	E95903	probable oxidoredu
87	273	21.0	268	2	G96016	probable gluconate
88	272.5	20.9	344	2	T44434	3-oxoacyl-(acyl-ca
89	272.5	20.9	246	2	A47542	short-chain alcoh
90	272	20.9	251	2	G73389	oxidoreductase, sh
91	272	20.9	263	2	S01227	glucose 1-dehydrog
92	272	20.9	319	2	S22416	3-oxoacyl-(acyl-ca
93	270.5	20.7	240	2	S75021	3-ketoacyl-acyl ca
94	270.5	20.7	261	2	S54815	uridamycin polyketi
95	270.5	20.7	262	2	D97325	3-oxoacyl-acyl car
96	269.5	20.7	260	2	G87408	gluconate 5-dehydr
97	269.5	20.7	261	1	S25079	monensin polyketid
98	269.5	20.7	265	2	C91254	probable sorbitol-
99	269	20.6	258	2	T51764	probable 2-hydroxy
100	269	20.6	257	2	F95284	probable [imported

Db 124 CSAVI-----RPMIKARSGAIYNISIVGLRSGSPGQTNAAAKGIIIGESKALSKEVGS 177  
QY 189 IGIRVMTIAPGLFGTPLLTSLPKVCNFIASQVFPSPRLGDPAE--YAHIVQAIINPFL 246  
Db 178 KNIRVNCIAPGFIIDMTKGLSDNKNEMLKGVPL-GRVGTPEIAMAALFLASNQSSYI 236  
QY 247 NGEVIRLDGAI 257  
Db 237 TGOVLSTVDGGM 247

Search completed: June 23, 2003, 14:29:23  
Job time : 9.8333 secs



OY 234 AHLVCAIENP---FLNGEYIRLDGAIRMQ 260  
 DB 222 AHLVCAFLADEKRGFTITGNEFYDGMATK 251

## RESULT 24

PHBB\_ALCEU STANDARD; PRT; 246 AA.  
 AC P14697;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Acetoacetyl-CoA reductase (EC 1.1.1.36).  
 GN PHBB.  
 OS Alcaligenes eutrophus (Ralstonia eutropha).  
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;  
 OC Ralstonia.  
 OX NCBI\_TaxID=510;

SEQUENCE FROM N.A.  
 RC STRAIN=H16 / DSM 428 / ATCC 17699;  
 RX MEDLINE=89359356; PubMed=2670935;  
 RA Peoples O.P., Sinskey A.J.;  
 RT "Poly-beta-hydroxybutyrate biosynthesis in Alcaligenes eutrophus H16.  
 RT Characterization of the genes encoding beta-ketothiolase and  
 RT acetoacetyl-CoA reductase."  
 RL J. Biol. Chem. 264:15293-15297(1989).  
 CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-CoA + NADPH.

CC -1- PATHWAY: Poly-beta-hydroxybutyrate biosynthesis; second step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: J04987; AAA21973.1; -  
 DR PIR: B34340; RDBLAB.  
 DR HSP: O70351; IE3S.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PRO0080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Oxidoreductase; NADP; PHB biosynthesis.  
 FT NP\_BIND 8 32 NADP (BY SIMILARITY).  
 FT ACT\_SITE 153 153 BY SIMILARITY.  
 SQ SEQUENCE 246 AA; 26370 MW; AD6739E0F5C93C06 CRC64;

Query Match 22.1%; Score 288.5; DB 1; Length 246;  
 Best Local Similarity 31.9%; Pred. No. 4,7e-15;  
 Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

OY 12 VAVITGASGLATLERLVGASAVLLDLPNSGGE---AQAKLGNVYFAPADVTS 67  
 DB 5 IAVTGGMGIGTALICORLAKDGFRRVAGCGSPRREKWLKQOKALGDFDIASEGNVAD 64  
 OY 68 EKDVOTLALAKGRFVDVAVNCAGIAVASKTYNLRKQOTHTLDFQRYLVNLMGTFN 127  
 DB 65 WDSKTRAFDKVSKSVGVVDVLLNAGI---TRDYVERK--MTRAWDVITDNLSTFN 118  
 OY 128 VIRLVAGEQNEPDGOGGQGVYIINTASVAEFGVQGAAYASAKSGIYGMILPIARDIA 187  
 DB 119 VTKQVIDGMA---DRGM--GRIVNISVNGQKGGQGTNYSTAKAGLHGFTALAQEVA 172  
 OY 188 PIGRWITNPGLEFGPRLTSLPEKCNFLASOVPPSPRLGDAFAHVLQALIT--ENPF 245

DB 173 TRGVTVNTVSPGYIATDWAKAIRQDVLDKIVATIPV-KRLGLPEIASIACAMLSSESGF 231  
 OY 246 LNGEYIRLDGAIRM 259  
 DB 232 STGADFSLNGGLHM 245

## RESULT 25

FABG\_CHLMU STANDARD; PRT; 248 AA.  
 AC O9PEF7;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-  
 DE acyl carrier protein reductase).  
 GN FABG OR TC0508.  
 OS Chlamydia muridarum.  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=83560;

SEQUENCE FROM N.A.  
 RC STRAIN=MOPN / N199;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.R., Peterson J., Ullrichback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Gwin M., Nelson W., Deboy R., Kolonay J., McClary G., Salberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RT "Genome sequences of Chlamydia trachomatis MOPN and Chlamydia  
 RT pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.

CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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DR EMBL: AE002319; AAF39350.1; -  
 DR HSP: P50163; ZAEI.  
 DR TIGR: TC0508; -  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PRO0080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.  
 FT NP\_BIND 12 36 NADP (BY SIMILARITY).  
 FT ACT\_SITE 157 157 BY SIMILARITY.  
 SQ SEQUENCE 248 AA; 25977 MW; 1F5C8968CB05FF58 CRC64;

Query Match 21.8%; Score 284.5; DB 1; Length 248;  
 Best Local Similarity 29.1%; Pred. No. 9,5e-15;  
 Matches 73; Conservative 48; Mismatches 111; Indels 19; Gaps 5;

OY 13 AVITGASGLGATLERLVGASAVLLDLPNSGGEARAK-----KLGNVYFAPADVTS 68  
 DB 10 ALVTGSGRIGGIGLAKLFAEAGANVQIWEAGKSAQDLSKTSKVSFAVDVSKN 69  
 OY 69 KDVTALALAKGRFVDVAVNCAGIAVASKTYNLRKQOTHTLDFQRYLVNLMGTFN 128  
 DB 70 DWVSAQVQKFLAEVGTIDVVVNNAGITRDSLLMMSSE-----EWSVSDITNIGSTYV 123  
 OY 129 IRLVAGEQNEPDGOGGQGVYIINTASVAEFGVQGAAYASAKSGIYGMILPIARDLAP 188

RC STRAIN-K12;  
 RX MEDLINE=97061202; PubMed=8905232;  
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Hojo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimura K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki Y., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiuchi T.,  
 RA "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome  
 RT corresponding to the 12.7-28.0 min region on the linkage map.";  
 RL DNA Res. 3:137-155(1996)  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) -> 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC PATHWAY.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M84991; AAA23739.1; -  
 DR EMBL; AE000210; AAC74177.1; -  
 DR EMBL; D90745; BAA35901.1; -  
 DR PIR; B42147; B42147.  
 DR HSSP; P29132; IDFI.  
 DR Ecocore: EGI1318; fabG.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PRO0080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.  
 FT NP\_BIND 10 34 NADP (BY SIMILARITY).  
 FT ACT\_SITE 151 151 BY SIMILARITY.  
 FT CONFLICT 30 30 A->G (IN REF. 1).  
 SQ SEQUENCE 244 AA; 25560 MW; 48ECLF2A7F7EEB9 CRC64;  
 Query Match 22.2%; Score 289.5; DB 1; Length 244;  
 Best Local Similarity 30.0%; Pred. No. 3.9e-15;  
 Matches 76; Conservative 50; Mismatches 112; Indels 15; Gaps 4;  
 QY 9 KGLVAVITGGASGLTAEELRVGOGASAVLLDLPNSGGEQAOKKGNVVFAPADTSE 68  
 DB 4 EGTALVTGASRGIGRAIAETLAARGAKVIGTATSENGAQSISYLLANGKGLMANTDP 63  
 QY 69 KDVOITALAKGKRGVDVAVNCAGIIVASKTYNKKKGOTHTLEDFORVLDVNLGTFNV 128  
 DB 64 ASISVLEKIRAEGERVDIVNAGITRDNLNLMKMO-----EEMWDIETNLSVERL 117  
 QY 129 IRLVAGEMGONEPDGOGRGVITNTASVAFEGOVGAASASGSGVGMTPILAPLAP 188  
 DB 118 SKAVRAMMKR-----RHGRITIGSVGTMGGANVAAAAGLIGFSKSLARFVAS 171  
 QY 189 IGRVMTIAPGLFTPLTSLPEKVCNFLASQVFPSPRLGDPAYALVO--AIIENPFL 246  
 DB 172 RGIIVNVVAPGFITDMTRALSDQGRAGILAQVP--ASRLGAGQIAVAVFLASDEAYI 230  
 QY 247 NGEVIRLDGAIRM 259  
 DB 231 TGETLVHNGMYM 243  
 RESULT 23  
 Y019\_THEME STANDARD; PRT; 256 AA.  
 AC Q56318;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative oxidoreductase TM0019 (EC 1.-.-.-).  
 GN TM0019.  
 OS Thermotoga maritima.  
 OC Bacteria; Thermotogae; Thermotogales;  
 OC Thermotogaceae; Thermotoga.  
 OX NCBI\_Taxid=2336;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MSB8 / DSM 3109;  
 RX MEDLINE=96125254; PubMed=8550425;  
 RA Kletzin A., Adams M.,  
 RT "Molecular and phylogenetic characterization of pyruvate and 2-  
 RT ketoisovalerate ferredoxin oxidoreductases from *Pyrococcus furiosus*  
 RT and pyruvate ferredoxin oxidoreductase from *Thermotoga maritima*.";  
 RL J. Bacteriol. 178:248-257(1996).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MSB8 / DSM 3109;  
 RX MEDLINE=9287316; PubMed=10360571;  
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
 RA Stewart A.W., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.K.;  
 RT Evidence for lateral gene transfer between Archaea and Bacteria from  
 RL genome sequence of *Thermotoga maritima*.  
 CC Nature 393:323-329(1999).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X65171; CA59459.1; -  
 DR EMBL; AE001690; AAD35113.1; -  
 DR HSSP; O70351; 1E6W.  
 DR TIGR; TM0019;  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PRO0080; SDRFAMILY.  
 KW Hypothetical protein; Oxidoreductase; NADP; Complete proteome.  
 FT NP\_BIND 9 33 NADP (BY SIMILARITY).  
 FT ACT\_SITE 153 153 RGGGVIT -> TRMRSDH (IN REF. 1).  
 FT CONFLICT 130 136 RGGGVIT -> TRMRSDH (IN REF. 1).  
 SQ SEQUENCE 256 AA; 28078 MW; D68160B1D7980C6B CRC64;  
 Query Match 22.2%; Score 289.5; DB 1; Length 256;  
 Best Local Similarity 31.1%; Pred. No. 4.1e-15;  
 Matches 84; Conservative 45; Mismatches 104; Indels 37; Gaps 8;  
 QY 8 VKGLVAVITGGASGLTAEELRVGOGASAVLLDLPNSGGEQAOKKGNVVFAPAD 64  
 DB 2 LERKVAVITGGGGGIGAAIAGLFAENGKMYVIAEIDEENGVERBELRRRGIDVYFVKVD 61  
 QY 65 VTSEKDVOTALAKGKRGVDVAVNCAGIIVASKTYNKKKGOTHTLEDFORVLDVNLG 124  
 DB 62 VADENSVMKMYRKTVEIYGGVDVLYNNAVMYSKIFE-----RPLEMERIVRYNLNG 115  
 QY 125 TENVIRLVAGEMGONEPDGOGRGVITNTASVAFEGOVGAQASASGSGVGMTPILAP 184  
 DB 116 PYICSRVCAEEMK-----RG--GVIIINASTRAQSEPDTEPYASKSGVLAHLHS LAV 169  
 QY 185 DLAPIGIRVMTIAPGLFT-----PLTSLPEKVCNFLASQVFPSPRLGDPAYE 233  
 DB 170 SISRYHIRVAVISPQWITSEWKKRSLRKKPDLRPIDHE-----QHP--AGRVGNPDLI 221

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DR EMBL: A600752; AAC07575.1; -  
DR HSSP: P50163; 2AE1.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short.1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.  
FT NP\_BIND 12 36 NADP (BY SIMILARITY).  
FT ACT\_SITE 157 157 BY SIMILARITY.  
SQ SEQUENCE 248 AA; 26867 MW; 5CFDE9B9AD3FC205 CRC64;

Query Match 22.4%; Score 291.5; DB 1; Length 248;  
Best Local Similarity 30.0%; Pred. No. 2.0e-15;  
Matches 77; Conservative 50; Mismatches 109; Indels 21; Gaps 6;

OY 8 VKGLAVITGASGLGATAEIRLVGOGASAVLLDLPNSGGEAOAKLGNVVE----APA 63  
DB 5 LQGVSLVTSSTGTRIGRAIKLASAGSYIITGSGERAKVAEEIAKYGKAGVEM 64  
OY 64 DYTEKDVQATALAKKRGKRVDAVAVCAIAVASKTYNKKQOTHTLEDFOVLDVNL 123  
DB 65 NLISEESINKAFEEIYVLVDGIDLVNNAGITRDKLELR-----SLDMEEVLKYNLT 118  
OY 124 GFNVIVRLVAGEMQNPDOGGOR-GVIINTASYAAFEQGVQAAVSASKGIYGMILPT 182  
DB 119 GTFIVLQNSLRKMK-----QRMGRIVNIVSSVVGTVGVNAGVSTKAAGLIGFTSL 171  
OY 183 ARDLAPGIRMTAPGLFGPLTSLPEKVCNPLASQVPPSPRLGPAAEYAHVQAII 242  
DB 172 AKELAPRVVLVNAVAPGRIETDMVAIVSEIKOKYKEOIPL-GRFGSPPEEVANVLELCS 230  
OY 243 N--PFLNGEIVRLDGAII 257  
DB 231 ELASTIGEIVTHVNGM 247

RESULT 21  
ID PHAB\_ACISP STANDARD; PRT; 248 AA.  
AC P50203:  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Acetoacetyl-CoA reductase (EC 1.1.1.36).  
GN PHAB.  
OS Acinetobacter sp. (strain RA3849).  
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;  
CC Acinetobacter.  
OX NCBI\_Taxid=472;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95362679; PubMed=7635832;  
RA Schembri M.A., Bayly R.C., Davies J.K.;  
RT "Phosphate concentration regulates transcription of the Acinetobacter  
polyhydroxyalkanoic acid biosynthetic genes";  
RL J. Bacteriol. 177:4501-4507(1995).  
CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) -> 3-oxoacyl-CoA + NADPH.  
CC -1- PATHWAY: Polyhydroxyalkanoic acid biosynthesis; second step.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SCR) FAMILY.  
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DR EMBL: U37761; AA99472.1; -  
DR HSSP: P19992; LHDC.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short.1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KW Oxidoreductase; NADP.  
FT NP\_BIND 9 33 NADP (BY SIMILARITY).  
FT ACT\_SITE 155 155 BY SIMILARITY.  
SQ SEQUENCE 248 AA; 26727 MW; 850E0DC659795123 CRC64;

Query Match 22.3%; Score 291; DB 1; Length 248;  
Best Local Similarity 31.9%; Pred. No. 3.1e-15;  
Matches 82; Conservative 47; Mismatches 104; Indels 24; Gaps 7;

OY 12 VAVITGASGLGATAEIRLVGOGASAVLLDLPNSGGEAOAK-----LGNNYFAPAD 64  
DB 6 VALVLTGALGIGSEICRQLVTAGYKIATVPRE--EDERQWLOSSEFQDSVDFVLT 63  
OY 65 VTSEKDVQATALAKKRGKRVDAVAVCAIAVASKTYNKKQOTHTLEDFOVLDVNL 124  
DB 64 LNHHEATAIADALAEGRVDVLVNNAGI--TRDAIFKK--MSYQMSQVIDTNLKT 117  
OY 125 TRNVIVRLVAGEMQNPDOGGORGYIINTASYAAFEQGVQAAVSASKGIYGMILPT 184  
DB 118 LFTVQPVFNKMLEQ-----KSGRVNIVSSVNGKQFGQANYSASKGIIGFTKALAQ 171  
OY 185 DLAPGIRMTAPGLFGPLTSLPEKVCNPLASQVPPSPRLGPAAEYAHVQAII--E 242  
DB 172 EGRSMICVNVAVPGTATPMTATMRDYIKSIEMQIPL-QRLAPAEIAAVMYLVSEH 230  
OY 243 NPFLNGEIVRLDGAIRM 259  
DB 231 GAVTGETLSINGLYM 247

RESULT 22  
ID FABG\_ECOLI STANDARD; PRT; 244 AA.  
AC P25716; P78221;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100) (3-ketoacyl-  
DE acyl carrier protein reductase).  
GN FABG OR B1093.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
CC Escherichia.  
OX NCBI\_Taxid=562;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX STRAIN=K12;  
RX MEDLINE=92210530; PubMed=1556094;  
RA Rawlings M., Cronan J.E. Jr.;  
RT "The gene encoding Escherichia coli acyl carrier protein lies within  
a cluster of fatty acid biosynthetic genes";  
RL J. Biol. Chem. 267:5751-5754(1992).  
CC [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=K12 / MG1655;  
RX MEDLINE=9746617; PubMed=9278503;  
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12";  
RL Science 277:1232-1244(1997).  
CC [3]  
RP SEQUENCE FROM N.A.

DR PIR: A28212; A28212.  
 DR PIR: A26938; A26938.  
 DR PIR: B37762; B37762.  
 DR HSSP: P19992; 1HDC.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Oxidoreductase; NAD; Bile acid catabolism; Multigene family.  
 FT NP\_BIND 7 13 NAD (POTENTIAL).  
 FT NP\_BIND 32 36 NAD (POTENTIAL).  
 FT ACT\_SITE 157 157 BY SIMILARITY.  
 FT CONFLICT 159 162 TSRA -> YGG (IN REF. 2).  
 SQ SEQUENCE 249 AA; 26658 MW; 084E380521D72C93 CRC64;

Query Match 22.5%; Score 293; DB 1; Length 249;  
 Best Local Similarity 30.8%; Pred. No. 2.2e-15;  
 Matches 82; Conservative 46; Mismatches 102; Indels 36; Gaps 9;

QY 8 VKGLVAVITGGASGLATAEKLVGOGASAVLDPNLSGE-----AQAKL---G 55  
 DB 4 VDDITITGGTGRIGFAAKFLFENGAKVSIF-----GETQEVDTALAQKELYPEE 57  
 QY 56 NNVPFADADYSEKDVOTALAKGKGRVAVNCAGIYVASKTYNLKGGTHLEDFQ 115  
 DB 58 EYLGFAF-DLTSRAVMAAVGTVAQKGRDLDMINNGITMNSVFSRSE-----EDFK 110  
 QY 116 RYLDVNLMTFNVIRLVAGEMGNEPDGQGVYITNTASYAALFEQGVQGAASAKGCI 175  
 DB 111 NMDINNVNGFN-----GAMSAYQCKKDKKOGIINTASVTGIYGLSGIGPTSAQV 164  
 QY 176 VGMFLPADIAPGLFETPLTSLPEKVCNFIASQVFPFSLDPAEYAHV---QAIINP 235  
 DB 165 IGLHGGREIRIRINIVGAVPGVDTDMTKGIPLEDYKLTLPN-KRMKPEBIAN 223  
 QY 236 LVQAIINPFLNG---EYIRLDGAIK 258  
 DB 224 -VYLFASDLASGITATISVDGAYR 248

## RESULT 19

FABG\_VIBHA  
 ID FABG\_VIBHA STANDARD: PRT: 244 AA.

AC P53336;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).  
 GN FABG.  
 OS Vibrio harveyi.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

OX NCBI\_TaxID=669;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=96134997; PubMed=8550484;  
 RA Shen Z., Byers D.M.;

RT "Isolation of Vibrio harveyi acyl carrier protein and the fabg, acpP, and fabf genes involved in fatty acid biosynthesis."  
 RL J. Bacteriol. 178:571-573(1996).

CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) -> 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC PATHWAY:  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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DR EMBL: U39441; AAC3589.1; -  
 DR HSSP: P19992; 1HDC.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Fatty acid biosynthesis; Oxidoreductase; NADP.  
 FT NP\_BIND 10 34 NADP (BY SIMILARITY).  
 FT ACT\_SITE 151 151 BY SIMILARITY.  
 SQ SEQUENCE 244 AA; 25519 MW; FC41A1C65B8C9AA CRC64;

Query Match 22.4%; Score 291.5; DB 1; Length 244;  
 Best Local Similarity 29.8%; Pred. No. 2.8e-15;  
 Matches 76; Conservative 51; Mismatches 113; Indels 15; Gaps 4;

QY 7 SVKGLVAVITGGASGLATAEKLVGOGASAVLDPNLSGEAOKKIGNNVVFAPADVT 66  
 DB 2 NLEGIATLVGASRGIGRAIALLVERGATVIGTTSBGAAAISETYIGENKGLALNVT 61  
 QY 67 SERDVOTALAKGKGRVAVNCAGIYVASKTYNLKGGTHLEDFQRYLDVNLMTGF 126  
 DB 62 DVESEIATLKTINDECGAIDLIVNNAGITRDMILRMKD-----DEMNDIINTNLTPY 115  
 QY 127 NVIRLVAGEMGNEPDGQGVYITNTASYAALFEQGVQGAASAKGCIYGMTLEPIARDL 186  
 DB 116 RMSKAVLRGMKMK-----RAGRILVNGSVGTMGAGGTNTAAKAGVIGFTKMAHEV 169  
 QY 187 APGIRVMTIAPGLFETPLTSLPEKVCNFIASQVFPFSLDPAEYAHV---QAIINP 244  
 DB 170 ASRGVAVNVAVAPGFIETDMTKALINDQRAATLSNP-AGRLDPEIRISAVVFLSPFA 228  
 QY 245 FLNGEYIRLDGAIK 259  
 DB 229 YITGETLVHNGGWM 243

## RESULT 20

FABG\_AQUAE  
 ID FABG\_AQUAE STANDARD: PRT: 248 AA.

AC O67610;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).  
 GN FABG OR AQ.1716.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;  
 OC Aquifex.

OX NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

RT "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus."  
 RL Nature 392:353-358(1998).

CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) -> 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC PATHWAY:  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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QY 243 NPFLNGEVIRLDG 255  
 Db 229 SSVYTCAGELAVDG 241

RESULT 17  
 Y4VI\_RHISN STANDARD; PRT; 548 AA.  
 ID Y4VI\_RHISN  
 AC 053217;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Putative short-chain type dehydrogenase/reductase Y4VI (EC 1.-.-.-).  
 GN Y4VI.  
 OS Rhizobium sp. (strain NGR234).  
 OC Plasmid sym PNCGR234.  
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 CC Rhizobiaceae; Rhizobium.  
 CX NCBI\_TaxID=394;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=97305956; PubMed=9163424;  
 RA Feilberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,  
 RA Perret X.;  
 RT "Molecular basis of symbiosis between Rhizobium and legumes.";  
 RT Nature 387:394-401(1997).  
 RL [2]  
 RL Genome Res. 6:590-600(1996).  
 RT "SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 -1- FAMILY. CONTAINS TWO DOMAINS."  
 CC (SDR) FAMILY. CONTAINS TWO DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL; Z68203; CA92424.1; ALT\_INIT.  
 CC DR EMBL; AE000101; AAB91897.1; -  
 CC DR HSP; P50163; ZAE1.  
 CC DR InterPro: IPR002198; ADH\_short.  
 CC DR Pfam: PF00106; adh\_short.2.  
 CC DR PROSITE; PS00061; ADH\_SHORT; 1.  
 CC KW Hypothetical protein; Oxidoreductase; Plasmid; Repeat;  
 CC MW Multifunctional enzyme.  
 CC FT DOMAIN 1 250 SHORT-CHAIN DEHYDROGENASE/REDUCTASE 1.  
 CC FT NP\_BIND 271 548 NAD OR NADP (BY SIMILARITY).  
 CC FT NP\_BIND 12 37 NAD OR NADP (BY SIMILARITY).  
 CC FT ACT\_SITE 154 154 BY SIMILARITY.  
 CC FT NP\_BIND 280 304 NAD OR NADP (BY SIMILARITY).  
 CC FT ACT\_SITE 420 420 BY SIMILARITY.  
 CC FT SEQUENCE 548 AA; 57593 MW; 393598C5DF17C23F CRC64;  
 SQ

Query Match 22.6%; Score 294.5; Db 1; Length 548;  
 Best Local Similarity 33.6%; Pred. No. 4.1e-15;  
 Matches 86; Conservative 41; Mismatches 100; Indels 29; Gaps 8;

QY 10 GIVAVITGGASGLAERLVOGASAVYLDLPNSGGEQAKRIGNVYFAADYTSER 65  
 Db 9 GRTLVVVGAGGIGRALVYDIFPANGDVYAVVLDPSGVITLIGNLPFGHLEVDVSRD 68

QY 70 DVQATLALAKGFGFVAVANCAGI-----AVASKTYLKKGQHTLEDQFVLDVLMGT 125  
 Db 69 DVVALRALLRKRSRIEVLVNMNGIGPTMAATADT-----ALEDFQALAINLVGA 119

QY 126 FNVLRLVAGENGONEPDGGGGRGVINTASYAAFEQGVGAAYASAKSGIVGMLPIARD 185  
 Db 120 YSVACEFAKLM---KPG-----AAIVNVAISLGLGNPKRSAYASAKGISIRKSLACR 171

QY 186 LAPGIRMTATAPLGFPLTLTSPEKY----CNFLASQVFPFRLDPAVEALYQ--A 239  
 Db 172 WASGRIFVTAAPVHVRPMAEL-ERAGKIDVSAIRRVPL-GRAPRDEIARAVRELA 229

QY 240 IIEENFLNGEVIRLDG 255  
 Db 230 SAQASYINGSTLVYDG 245

RESULT 18  
 BA71\_EUBSP STANDARD; PRT; 249 AA.  
 ID BA71\_EUBSP  
 AC P07914;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) (Bile acid  
 DE 7-dehydroxylase) (7-alpha-HSDH) (Bile acid-inducible protein).  
 GN BA1A1 AND BA1A3.  
 OS Eubacterium sp. (strain VPI 12708).  
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 CX NCBI\_TaxID=29347;  
 RN [1]  
 RP SEQUENCE FROM N.A. (BA1A3).  
 RA MEDLINE=90330548; PubMed=2376563;  
 RA Gopal-Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.;  
 RT "Multiple copies of a bile acid-inducible gene in Eubacterium sp.  
 RT strain VPI 12708.";  
 RT J. Bacteriol. 172:4420-4426(1990).  
 RL [2]  
 RL SEQUENCE FROM N.A. (BA1A1).  
 RX MEDLINE=88197993; PubMed=2834320;  
 RA Coleman J.P., White W.B., Lijewski M., Hylemon P.B.;  
 RT "Nucleotide sequence and regulation of a gene involved in bile acid  
 RT 7-dehydroxylation by Eubacterium sp. strain VPI 12708.";  
 RT J. Bacteriol. 170:2070-2077(1988).  
 RN [3]  
 RP SEQUENCE OF 1-55 FROM N.A. (BA1A1), AND SEQUENCE OF 1-33.  
 RX MEDLINE=87165759; PubMed=3549693;  
 RA Coleman J.P., White W.B., Hylemon P.B.;  
 RT "Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp.  
 RT strain VPI 12708.";  
 RT J. Bacteriol. 169:1516-1521(1987).  
 CC -1- FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID, YIELDING  
 CC DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST  
 CC AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID.  
 CC -1- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-  
 CC cholanate + NAD(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-  
 CC cholanate + NADH.  
 CC -1- PATHWAY: Bile acid catabolism.  
 CC -1- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A  
 CC 7-ALPHA-HYDROXY GROUP.  
 CC -1- SIMILARITY: THERE ARE THREE GENES FOR BA1A PROTEINS. BA1A1 IS  
 CC IDENTICAL TO BA1A3 AND THERE IS 81% IDENTITY WITH BA1A2.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; M34658; AAB61155.1; -  
 CC DR EMBL; M19654; AAB61154.1; -  
 CC DR EMBL; M15813; AAB61153.1; -

RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunet F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azavedo J., Bortner M.G., Bessieres P., Bolotin A., Borcher S.,  
 RA Bortner R., Bortner L., Bortner M., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruscia C.V., Caldwell B., Capuano N.J., Carter N.M.,  
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings V., Daniel R.A.,  
 RA Dentzov F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Entian K.D., Erington J., Fabret C., Ferrati E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallazzi A., Galleron N.,  
 RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Iraya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klier-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Mestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogasawa K., Ogihara A., Oudeg B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetalle D., Porroli S., Prescott A.M.,  
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Ray M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Schreier R., Scoffone F.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Taccori E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tononi A.,  
 RA Tostato V., Uchiyama S., Vandenberg M., Vamler F., Vassarotti A.,  
 RA Viari A., Wambolt R., Wedler E., Welteregger T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Darchin A.,  
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*  
 RT *subtilis*.";  
 RT NATURE 390:249-256(1997).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
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 CC -----  
 DR EMBL: X73124; CA51638.1; -  
 DR EMBL: 299123; CA515799.1; -  
 DR PIR: S39737; S39737.  
 DR HSP: P50163; IAE1.  
 DR Subtilisin, BGI0628; yfD.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR PRINTS: PRO0080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT.1.  
 DR Hypothetical protein: Oxidoreductase; Complete proteome.  
 KM NP\_BIND 11 33 NAD OR NADP (BY SIMILARITY).  
 FT ACT\_SITE 154 154 BY SIMILARITY.  
 FT SEQUENCE 255 AA; 27324 MW; 20AA2235BFB869B CRC64;

Query Match 23.1%; Score 301; DB 1; Length 255;  
 Best Local Similarity 32.7%; Pred. No. 5,6e-16;  
 Matches 88; Conservative 42; Mismatches 93; Indels 46; Gaps 8;  
 Oy 14 VITGGASGLGTAERLVGOGASAVLLDLPNSGGEQAKKLGNN-VYFADYTSKDVQ 72  
 Db 11 LITGGASGIGYAVVQFLGQAVNVVADIDEAGGEAVKRENDRIHEVQDTITDEAQC 70  
 Oy 73 TALALAKGKRGYDVAVNCAGIYVASKTYNLKKGQHTLEDFOFVLDVNLGTFNIR-- 130  
 Db 71 HAYEASVHTFGGLDVLINNGAGIYVPIHENE-----LSDMKVLQVNLTGFLMSKIA 124  
 Oy 131 ----LVAGEGQNEPDGQGGVYINTASVAAFEGVGGAASASAGGIVGKTLPIARDL 186  
 Db 125 LKHLALAG-----KGNINTCVSGGLVAMPDIPATYNAKGGVQLTKMSAVDY 172

Oy 187 APGIRVMTAPGLFGLPLTSLPEKVCNLF-----ASGVPPSLGDPAY 233  
 Db 173 AKHGVNVCVCPGIIIDP-----LNKE--SFLENNGTLEIRKREKAKVNLRLRGPEEL 226  
 Oy 234 AHVQALIE--NPLNGEVIRLDGAIMQ 260  
 Db 227 ANVMLFASLDLSYMTGSATADGCTTAQ 255  
 RESULT 16  
 2BHD\_STREX STANDARD: PRT: 255 AA.  
 ID 2BHD\_STREX  
 AC P19992 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).  
 OS Streptomyces exfoliatus (Streptomyces hydrogans).  
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;  
 OC Actinomycetales; Streptomyces; Streptomyces; Streptomyces.  
 CX NCBI\_TaxID=1905;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90306362; PubMed=2194840;  
 RA Marekov L., Krook M., Joernvall H.,  
 RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the  
 RT 'short-chain, non-metalloenzyme' alcohol dehydrogenase type.";  
 RL FEBS Lett. 266:51-54(1990).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RX MEDLINE=92052211; PubMed=1946424;  
 RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,  
 RA Rimsay R.L., Orr J.C.;  
 RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid  
 RT dehydrogenase: a member of a short-chain dehydrogenase family.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).  
 CC -1- CATALYTIC ACTIVITY: Androstane-3-alpha,17-beta-diol + NAD(+) = 17-  
 CC beta-hydroxyandrostane-3-one + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 DR PIR: S10707; S10707.  
 DR PDB: ZHSD; 31-AUG-94.  
 DR PDB: LHDC; 07-FEB-95.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR PRINTS: PRO0080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT.1.  
 KM NP\_BIND 10 34 NAD (BY SIMILARITY).  
 FT ACT\_SITE 152 152  
 FT SEQUENCE 255 AA; 26484 MW; 9CB93CB66AA628D5 CRC64;

Query Match 22.9%; Score 299; DB 1; Length 255;  
 Best Local Similarity 33.6%; Pred. No. 7,9e-16;  
 Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;  
 Oy 8 VGLVAVITGGASGLGTAERLVGOGASAVLLDLPNSGGEQAKKLGNNVYFADYTS 67  
 Db 4 LSGKTVIITGGARGGAEARQAVAGARVYLDVDEGATARELDAAAYQHTDVTI 63  
 Oy 68 EEDVOTATLALAKGKRGYDVAVNCAGIYVASKTYNLKKGQHTLEDFOFVLDVNLGTFN 127  
 Db 64 EEDMORVAVAYAEESGSDGLVNNAGISTGFL-----EESVREKRYVDINTLGVFI 117  
 Oy 128 VITLVAGEGQNEPDGQGGVYINTASVAAFEGVGGAASASAGGIVGKTLPIARDLA 187  
 Db 118 GKRTIYIPAV---KDAAG--GSIVNISAAGIMGIALTSSGASKMGVRLSKLAAYELG 171  
 Oy 188 PIGIVVMTAPGLFGLPL--TSLPEKVCNLFASVPPSLG--DPAVYALVQALIE-- 242  
 Db 172 TDRIRVNSVHPKMTYPTAETGIRQGGNT--PNTPR--GRVGNBGEIACAAVVKLSDT 228

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FT NP_BIND 9 33 NADP (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
FT CONFLICT 23 23 D -> A (IN REF. 1).
SO SEQUENCE 246 AA: 26282 MM: C6A91167D9237DC CRC64:

Query Match 23.7% Score 309.5, DB 1, Length 246:
Best Local Similarity 29.7% Pctd. No. 1,2e-16;
Matches 76: Conservative 55; Mismatches 100; Indels 25; Gaps 6;

QY 13 AVITGGSGAGLTAETRLVGASAVYLDLPNSGGEAOA-----KTLGNNAVFPADY 65
Db 7 AITVTGASRGIGRSLADLAKSGANV---VNSGNEKANEVDEIKSMGRKAIANKADY 63
QY 66 TSEKDVOTALALAKKFGKRVDAVNCAGIAVASKTYNKKGGTHLTEDFORIVDNLMT 125
Db 64 SNPEVDNMMKIKETLSVFSTIDILVNNNGITRDLINMKKE-----DEMDVDVINILKGY 117
QY 126 FNYVRLVAGMGQNEPDDGGORGVIINTASVAAPFEGOVGAASASKGIIVGTLPIARD 185
Db 118 FNCRKATRTQMKQ-----RSGRILNVSSIVGSGNPGGANVAAKAGVIGLTKSSAKE 171
QY 186 LAPIGIKVMTIAPGLFSTPLTISLPEVCNCFLASQVFPSPRLDDPAFYATNVALIEN-- 243
Db 172 LASRNIVNAIAPFISTDMTDKIAKVQDEMLKQIPL-ARFEPSPDVSSVTFILASEGA 230
QY 244 PELNGEVIIRLDGAIRM 259
Db 231 RYMGTGQTLHDGMYM 246

RESULT 14
YK02_MYCTU YK02_MYCTU STANDARD: PRT: 260 AA.
AC Q10855;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase Rv2002 (EC 1.-.-.-).
GN FABG3 OR RV2002 OR MT2058 OR MTCY39.16C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteriidae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CX NCBI_Ltaxid=1773;
CY [1]
RC SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RC MEDLINE=98295987; PubMed=9634230;
RX Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagers K., Krogh A., McLean J., Moile S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RL complete genome sequence."
RN Nature 393:537-544(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmailova M.D., Salzberg S.L.,
RA Delcher A., Ditterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RL laboratory strains."
RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
DR EMBL; 274025; CAA98414.1; -
DR EMBL; AE007057; AAK4635.1; -
DR HSPG; P19992; IHDC.
DR TIGR; M20058; -
DR TubercuList; RV2002; -
DR InterPro; IPRO02198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
FW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
KW NP_BIND 11 35 NAD (BY SIMILARITY).
FT ACT_SITE 153 153 BY SIMILARITY.
FT CONFLICT 174 174 S -> G (IN REF. 2).
SQ SEQUENCE 260 AA; 27030 MW; 0935A14ED36220B7 CRC64;

Query Match 23.4%; Score 305; DB 1; Length 260;
Best Local Similarity 33.9%; Pred. No. 2.8e-16;
Matches 85; Conservative 41; Mismatches 99; Indels 26; Gaps 5

QY 10 GLVAVITGSGAGSGLIATRELVGQGSASVLLDLPNSGGEAOAKLGNVVFAPADYTSER 69
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 7 GKVALVSGGARGSGASHVAMAEKAKVFFGDIIDESEKNAVAALADAAVYHLDYTPA 66
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 DVQATALAKGKFGKRVDAVNCAGIAVASKYINLKKGQTHLEDFQRYLDVNLGTFNYI 129
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 67 QWTAADVTATATGAGLHVLYNNAGI-----LNTGTTEDVATLTWQRIPLVNLGVFLGI 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 RLVAVGEGNQEPPOGQGRGRIIVINTASVAAFEGOVQAQASAKGIGYMTLPINRDIAP 189
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 RAVY-----KPKKEKRGRSIIINISIEBLAGTVACHGYTKFRAVAGLKRSTALEGPS 174
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 GIRVMTAPLEFECTPLILTSLEPKVCNLFASQVFPSPSLG---DAEFAHLV--QALLENP 244
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 175 GIRVNSIHPLEIVTPTMTDWPEDI-----FQTALGRAAEPEVSNLVIYLADESS 225
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 245 FLNGEVIRLDG 255
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 226 YSTGAERFYVDG 236
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
YWFD_BACSU
ID YWFD_BACSU STANDARD; PRT; 255 AA.
AC P39640;
DT 01-PEB-1995 (Rel. 31, Created)
DT 01-PEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical oxidoreductase ywfD (C1.-...).
DE ywfD OR IPA-82D.
GN Bacillus subtilis.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RC MEDLINE=95020537; PubMed=7934828;
RA Glaser P., Kunst F., Arnold M., Coudart M.P., Gonzales W.,
RA Hullo M.E., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
RA Pirescan E., Santana M., Schneider E., Schweizer U., Verres A.,
RA Rapoport G., Danchin A.;
RT "Bacillus subtilis genome project: cloning and sequencing of the 97
RT kb region from 325 degrees to 333 degrees.";
RL Mol. Microbiol. 10:371-384(1993).
RN
RC SEQUENCE FROM N.A.
RC STRAIN=168;

```



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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: U34072; AAC53573.1; -  
 DR EMBL: U34072; AAC53574.1; -  
 DR EMBL: AF100956; AAC69902.1; -  
 DR HSSP: 070351; 186M.  
 DR MGD: MGI:95911; H2-Re6.  
 DR InterPro: IPR002198; ADH\_Short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 KM Steroid biosynthesis; Oxidoreductase; NAD; Multigene family;  
 KM Alternative splicing.  
 FT NP\_BIND 13 38 NAD (BY SIMILARITY).  
 FT ACT\_SITE 168 168 BY SIMILARITY.  
 FT VAREPLIC 257 260 GLEM -> MRSWGGGCGENTQVYMRK (IN LONG  
 FT CONFLICT 16 16 ISOFORM)  
 FT CONFLICT 17 17 G->GSVPSQ (IN REF. 3).  
 FT CONFLICT 230 230 MISSING (IN REF. 1).  
 FT CONFLICT 230 230 E->EG (IN REF. 1).  
 SQ SEQUENCE 260 AA; 26645 MW; 19C712FCDD168B08 CRC64;

Query Match 24.0%; Score 313.5; DB 1; Length 260;  
 Best Local Similarity 31.0%; Pred. No. 6.4e-17;  
 Matches 85; Conservative 54; Mismatches 106; Indels 29; Gaps 9;

OY 1 MAACRSYKGLVAVITGCA-SGLGIAFAERLVGGASAVLLDPNSGGEQAQKIGN-- 56  
 DB 1 MASOLR-LRSALALVTGGAGSGISRAISVRLAAGAAVAACDLDGAAGQTVRLGSPGS 59  
 OY 57 -----NVYFAADYTSKEDVOTATLAKGKGR--VDVAVNAGIAVASKITNKKQ 107  
 DB 60 EDGAPRGHAAAF-QADVSQGPAAARLLBEVQACSRPPSVVSCAGITRDEFLHMS- 116  
 OY 108 THLEDFQRLVDVNLMTGFENVIRLVAGEMGNEPDGQGRVINTASVAAFEGOVQAA 167  
 DB 117 ----EDMDRVIAVNLKGTFLVYTAQAQALVSS-----GGROSINISITIGKVNIGQTN 167  
 OY 168 YSASKGIVGKTLTADLAPIGIRVFIAGLFGTLLSLSPKVCNFIASQVPPPSRL 227  
 DB 168 YASSRAGVIGLQPAARLGRHGRCSVLPGLFATPTOMPKVADKVTAMIP-L-GHM 226  
 OY 228 GDPAEVYALVQ--AIENPFLNGEVIRIDGAIIR 259  
 DB 227 GDPEDVADVAVFLASEDSGYITGASVEVSGGLFM 260

RESULT 13  
 FABG\_BACSU STANDARD; PRT: 246 AA.  
 ID FABG\_BACSU  
 AC P51831; G31733;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-  
 DE acyl carrier protein reductase).  
 GN FABG.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RA MEDLINE=96326321; PubMed=8759840;  
 RA Mordiment H.R., de Mendoza D., Cronan J.E. Jr.,  
 RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of  
 RT lipid biosynthesis genes";  
 RL J. Bacteriol. 178:4794-4800(1996).

RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Aevedo V., Bertorello M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Boursier L., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Ertlin K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
 RA Guilseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klier-Bianchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Prescan E., Puig P., Purnelle B., Rapoport G., Ray M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Serot S.J., Serot P., Shin B.S., Solido B.,  
 RA Sorokin A., Taccout E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Takamashi A., Tanaka T., Terpstra P., Tognoni A.,  
 RA Tostato V., Uchiyama S., Vandenbol M., Vanlier F., Vassart A.,  
 RA Viart A., Wambutt R., Wedler E., Wedler H., Welzenegger T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yatsunoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,  
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
 RT subtilis";  
 RL Nature 390:249-256(1997).  
 RN [3]  
 RP SEQUENCE OF 1-172 FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98195738; PubMed=9534248;  
 RA Foulger D., Errington J.;  
 RT "A 28 kbp segment from the spvA region of the Bacillus subtilis 168  
 RT genome";  
 RL Microbiology 144:801-805(1998).  
 RN [4]  
 RP SEQUENCE OF 230-246 FROM N.A.  
 RC STRAIN=168;  
 RA Oguero A., Kakeshita H., Takamatsu H., Nakamura K., Yamane K.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 CC CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC PATHWAY.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
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CC EMBL: U59433; AAC44307.1; -  
 DR EMBL: Z99112; CAB13464.1; -  
 DR EMBL: Y13937; CAI/4250.1; -  
 DR EMBL: D64116; BAA10974.1; -  
 DR HSSP: Q12634; 1YBV.  
 DR Subtilist: BGI1535; fabG.  
 DR InterPro: IPR002198; ADH\_Short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; FALSE\_NEG.  
 KM Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.



```

Db      62  NPSISIAVLKAIINDEGGVDILVNNAGITRDLLMRKE-----EEMSDIMETNLSIF 115
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      127  NVIRLVAGEMGQNEPQGGQGRVITINTASVAFEEQVQGAQYSAKSGIVGNTLPIARDL 166
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      116  RLSKAVLVGRMKK-----RGRRIINVGSVGTGMNAQANVAAKAGVIGFTSMARV 169
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      187  APIGIRVMTIAPGLFETPLLTSLPERKVCNTLSQVFPFSRLDGPDAEYAHVLQAIIEP-- 244
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      170  ASRGVIVYNTVAPFETIDMTKALNDEQRATLQVY-AGRLGDPREINSAV-ATLASPEA 227
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      245  -FLNGEYIRLDGARIM 259
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      228  AYTIGETLHVNGGNYM 243
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

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RESULT 11			
FAG1_SYNV3	STANDARD;	PRT;	247 AA.
AC	P73574;		
DT	15-DEC-1998 (Rel 37, Created)		
PT	15-DEC-1998 (Rel 37, Last sequence update)		
DT	16-OCT-2001 (Rel 40, Last annotation update)		
DE	3-oxoacyl:lacyl carrier protein reductase 1 (EC 1.1.1.100) (3		
DE	ketoadyl:lacyl carrier protein reductase 1).		
GN	FAG1L OR SLR0886.		
OS	<i>Synechocystis</i> sp. (strain PCC 6803).		
OC	Bacteria; Cyanobacteria; Chroococcales; <i>Synechocystis</i> .		
OX	NCBI_TaxID=1148;		

RP SEQUENCE FROM N.A. PubMed=8905331:  
RX MEDLINE-97061201:  
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
RA Miyajima N., Hirosewa M., Sugura M., Sasamoto S., Kimura T.,  
RA Hoshouchi T., Matsuo A., Murai A., Nakazaki N., Natuo K., Okumura S  
RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M.,  
RA Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DN. Res. 3:109-136(1996).  
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
CC PATHWAY.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY.

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DR EMBL: D90907; BAA17614.1; -  
DR HSSP: P50162; 1AE1  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short; 1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KW Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome  
FT NP\_BIND 11 35 NADP (BY SIMILARITY).  
FT ACT\_SITE 156 156 BY SIMILARITY.  
SQ SEQUENCE 247 AA; 25724 MW; 91B5F9409C777F20 CRC64;

Query Match	24.0%	Score 313.5	DB 1	Length 247
Best Local Similarity	32.1%	Pred. No. 6.1e-17		
Matches 85	Conservative 45	Mismatches 92	InDels 43	Gaps 8

QY 12 VAVITGASGLATAPRLVGQ-----ASAVLLDLPNSGGGAQAKKIGNV 58  
||::|| : ||| || | ||::: : ||||

[illegible]

ID	DBH8_MOUSE	STANDARD:	PRT:	260 AA.
AC	P50171;	Q60959;	Q60958;	Q921W2:
DT	01-OCT-1996	(Rel. 34,	Created)	
DT	01-OCT-1996	(Rel. 34,	Last sequence update)	
DT	16-OCT-2001	(Rel. 40,	Last annotation update)	
DE	Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-beta-hydroxysteroid dehydrogenase 8) (K6 protein) (Ke-6).			
GN	HS17B8 OR HKE6 OR H2-K6.			

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathae; Muridae; Mus  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney.  
RX MEDLINE=93180832; PubMed=8441417;  
RA Azziz N., Maxwell M.M., St Jacques B., Brenner B.M.;  
RT "Downregulation of Ke 6, a novel gene encoded within the major  
RT histocompatibility complex, in murine polycystic kidney disease."  
RL *Mol. Cell. Biol.* 13:1847-1853(1993).

RA Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;  
 RE KRAVITZ.  
 RL Moll. Cell. Biol. 13:6614-6614(1993).  
 RN [3].  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6;  
 RX MEDLINE=96027630; Pubmed=7559658;  
 RA Maxwell M.M., Nearing J., Aziz N.;  
 RT "K6 gene. Sequence and organisation and aberrant regulation in  
 RL murine polycystic kidney disease." J. Biol. Chem. 270:25213-25219(1995).

CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.  
CC NAD(P)H.  
RT Submitted (OCT-1998) to the EMBL/Genbank/CDR database.  
RI -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.  
CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)<sup>(+)</sup> = estrone +  
RT "sequence of the mouse major histocompatibility locus class II  
RA Hall T., Lasky S., Madan A., Loretz C., James R., Dots M., Mix L.,  
RC ROVEN L., Qin S., Madden A., Lorenz C., James R., Dots M., Mix L.,  
RP STRAIN-129/SVJ;  
PP SEQUENCE FROM N.A.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A SHORT FORM (SHOWN HERE) AND A LONG FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: KIDNEY, LIVER AND MODERATELY IN SPLEEN, HEART AND BRAIN.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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AC 092506;90U01; 30-MAY-2000 (Rel. 39, Created)
AD 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE beta-hydroxysteroid dehydrogenase 8 (Ec 1.1.1.62) (17-beta-HSD 8) (17-
GN HSD17B8 OR HKE6 OR RING6 OR FABGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tubby B.;
RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-261 FROM N.A.
RX MEDLINE=97001166; PubMed=8812499;
RA Ando A., Kikuchi Y., Shigenari A., Kawata H., Okamoto N., Shilina T.,
RA Chen L., Ikemura T., Aoe K., Kimura M., Inoko H.;
RT "cDNA cloning of the human homologues of the mouse Kε4 and Kε6 genes
RT at the centromeric end of the human MHC region.";
RL Genomics 35:600-602(1996).
CC -1 FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
CC -1 CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +
CC NAD(P)H.
CC -1 PATHWAY: BIOSYNTHESIS OF ESTROGENS.
CC -1 TISSUE SPECIFICITY: HIGH EXPRESSION IN THE LIVER AND PANCREAS,
CC LOWER IN THE SKELETAL MUSCLE AND KIDNEY.
CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SBR) FAMILY.
CC -----
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CC -----
CC CC
CC DR EMBL; AL031228; CAC38444.1; -
CC DR EMBL; D82061; BAAL1529.1; -
CC DR HSSP; O70351; 186W.
CC DR Genew; HGNC:3554; HSD17B8.
CC DR MIM; 601417; -
CC DR InterPro; IPR002198; ADH_short.
CC DR Pfam; PF00106; adh_short; 1.
CC DR PRINTS; PR00080; SDRFAMILY.
CC DR PROSITE; PS00061; ADH_SHORT; 1.
CC KW Steroid biosynthesis; Oxidoreductase; NAD; Multigene family.
CC FT NP_BIND 15 39 NAD (BY SIMILARITY).
CC FT ACT_SITE 169 169 E -> R (IN REF. 2).
CC FT CONFLICT 117 117 E -> R (IN REF. 2).
CC FT CONFLICT 193 193 R -> P (IN REF. 2).
CC FT CONFLICT 208 208 Q -> K (IN REF. 2).
CC FT CONFLICT 212 212 Q -> K (IN REF. 2).
CC SQ SEQUENCE 261 AA; 26974 MW; 8B8BD7131714D71 CRC64;
CC -----
QY Query March 25.5%; Score 332.5; DB: 1; Length 261;
Db Best local similarity 31.2%; Pred. No 2.4e-18;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
QY 8 VKGLAVITGGASGLGATAERLVGGAGASAVYLDLPNSGGEQAQKLT-----GN 56
Db 1RSALATLVYTAGSSIGRAVSYRLAGEGATVACDLPAAQETVRLILGGSPGKPPGN 68
QY 57 NVYAPAPADVSEKQVQVQFALAKKQKGR-VDVAVNCGCIANASTYNNLKQGTHTLDPQ 115
Db 69 HAAF-QADVSEARARCLLEGVQVQCFSRPSPSVVSCAGITODEFLHMSR-----DDWD 121
QY 116 RVLVDNVLGTFNNYIRLVAGENGQNEPDQGGQGVYINTASVAFEGQVQQAAYSASKGI 175
Db 122 KVLIVNFKGTFVLVYQAQAALVSN-----GGRGSIINISLIVGKVGANNQINNYAASKAGV 176

```

[illegible]

RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,  
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson M.C., Ketchum K.A.,  
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 genome sequence of *Thermotoga maritima*.";  
 Nature 399:323-329 (1999).  
 CC -1- CARBAMYLIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC PATHWAY.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
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 CC -----  
 CC EMBL: A601811; AAD36790.1; -  
 CC HSSP: P50162; 1AEL.  
 CC TIGR: TM1724; -  
 CC InterPro: IPR002198; ADH\_short.  
 CC Pfam: PF00106; adh\_short; 1.  
 CC PRINTS: PR00080; SDRFAMILY.  
 CC PROSITE: PS00061; ADH\_SHORT; 1.  
 CC Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.  
 CC NP\_BIND 10 NADP (BY SIMILARITY).  
 CC ACT\_SITE 154 154 BY SIMILARITY.  
 CC SEQUENCE 246 AA; 806804D28099142 CRC64;  
 SQ  
 Query Match 26.5%; Score 346; DB 1; Length 246;  
 Best Local Similarity 34.1%; Pred. No. 2.1e-19;  
 Matches 87; Conservative 47; Mismatches 103; Indels 18; Gaps 5;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Myrtales; Lythraceae; Cuphea.  
 OC NCBI\_TaxID=3930;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9229104; PubMed=1376402;  
 RA Klein B., Pawlowski K., Hoerlcke-Grandpierre C., Schnell J.,  
 RA Toepfer R.,  
 RT "Isolation and characterization of a cDNA from *Cuphea lanceolata*  
 RT encoding a beta-ketoacyl-ACP reductase.";  
 RL Mol. Gen. Genet. 233:122-128 (1992).  
 CC -1- CARBAMYLIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC PATHWAY.  
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC  
 CC PLASTIDS.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: X64566; CAA45866.1; -  
 CC FIR: S19832; S19832.  
 CC HSSP: P50162; 1AEL.  
 CC InterPro: IPR002198; ADH\_short.  
 CC Pfam: PF00106; adh\_short; 1.  
 CC PRINTS: PR00080; SDRFAMILY.  
 CC PROSITE: PS00061; ADH\_SHORT; 1.  
 CC Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast;  
 CC Transit peptide.  
 CC TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).  
 CC CHAIN 62 320 3-OXOACYL-[ACYL-CARRIER PROTEIN]  
 CC FT NP\_BIND 82 106 REDUCTASE.  
 CC FT ACT\_SITE 227 227 NADP (BY SIMILARITY).  
 CC SEQUENCE 320 AA; 33103 MW; 06BAF0522B28C87 CRC64;  
 SQ  
 Query Match 25.6%; Score 334; DB 1; Length 320;  
 Best Local Similarity 32.7%; Pred. No. 2.3e-18;  
 Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;

OC RESULT 8  
 OC FARG\_CUPHA STANDARD; PRT; 320 AA.  
 ID FARG\_CUPHA  
 DB 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor  
 DE (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).  
 GN CLKR27.  
 OS Cuphea lanceolata.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC RESULT 9  
 OC DHB8\_HUMAN STANDARD; PRT; 261 AA.  
 ID DHB8\_HUMAN  
 DB 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor  
 DE (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).  
 GN CLKR27.  
 OS Cuphea lanceolata.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA;  
 RA Fu J., Chen X., Stern D., Yan S.D.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U96116; AB57689.1; ALT\_INT.  
 DR HSBP: Q70351; 186M.  
 DR SWISS-2DPAGE: O08756; MOUSE.  
 DR MGI: MGI:133871; Hsd17b10.  
 DR InterPro: IPR002198; ADH\_Short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Oxidoreductase; NAD.  
 KW NP\_BIND 12 NAD (BY SIMILARITY).  
 FT ACT\_SITE 168 168 BY SIMILARITY.  
 FT SEQUENCE 261 AA; 27418 MW; 6121381352839D41 CRC64;  
 SQ  
 Query Match 86.0%; Score 1122; DB 1; Length 261;  
 Best Local Similarity 85.8%; Pred. No. 4.7e-78;  
 Matches 224; Conservative 19; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 MAACRSYKGLVAVITGASGLGATARLVGCGASAVILDLPSGGEAAKXKGNVVF 60  
 DB 1 MAARSVKGLVAVVTTGASGPMPLATKRLVGGATALLVDPSEGGSAKKLGESCIF 60  
 QY 61 APADYSEKDVQATALALAKGKFGKRVAVNACGIAVASKTYNKKGGTHLEDFQRLVDV 120  
 DB 61 APANTSKSEKQALALTLAKKEKFRDVAVNACGIAVAKTKYHKKKTHLEDFQRYINV 120  
 QY 121 NLMGFNVIKLVAGMGNGNEPDGQGRVITNTASVAFEEQVQCAAYSAKSGIVMTL 180  
 DB 121 NLIGFNVIKLVAGMGNGNEPDGQGRVITNTASVAFEEQVQCAAYSAKSGIDKTL 180  
 QY 181 PIARDIAPIGIRVMTIAPLGTPLTSLPKVCNFTLASQVFPFSRLDPAEYVAHLYOAI 240  
 DB 181 PIARDIAPIGIRVMTIAPLGTPLTSLPKVCNFTLASQVFPFSRLDPAEYVAHLYOAI 240  
 QY 241 IENPLNGEVIRLDGAIKMP 261  
 DB 241 IENPLNGEVIRLDGAIKMP 261  
 RESULT 5  
 HCD2\_DROME STANDARD: PRT: 255 AA.  
 ID HCD2\_DROME  
 AC 018404;  
 DT 16-OCT-2001 (Rel. 40; Created)  
 DT 16-OCT-2001 (Rel. 40; Last sequence update)  
 DT 16-OCT-2001 (Rel. 40; Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
 DE (Scully protein).  
 GN SCU OR CG7113.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND MUTAGENESIS OF LEU-33 AND PHE-120.  
 RC STRAIN= Canton-S;  
 RX MEDLINE=98252852; PubMed=9585418;  
 RA Torroja L., Ortuno-Sahagun D., Ferrus A., Haemmerle B., Barbas J.A.;  
 RT Scully, an essential gene of Drosophila, is homologous to mammalian  
 RT mitochondrial type II L-3-hydroxyacyl-CoA dehydrogenase/amyloid-beta  
 RT peptide-binding protein.  
 RT J. Cell Biol. 141:1009-1016(1998).  
 RL  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN= Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.C., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brannon R.C., Rogers Y.H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,  
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Dey A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Gary N.S., Galbati W.M., Glasser K.,  
 RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyan C.,  
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Schaefer F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Styksas R., Tector C., Turner R., Venler E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RL "The genome sequence of Drosophila melanogaster."  
 CC Science 287:2185-2195(2000).  
 CC -1- FUNCTION: MAY PLAY A ROLE IN GERM LINE FORMATION.  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC -1- SUBUNIT: MULTIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (BY similarity).  
 CC -1- TISSUE SPECIFICITY: FOUND IN MANY TISSUES INCLUDING CNS. HIGHEST  
 CC EXPRESSION IN BOTH EMBRYONIC GONADAL PRIMORDIA AND MATURE OVARIES  
 CC AND TESTES.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
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CC EMBL; AB002156; BAA19510.1; -  
CC HSSP; O70351; 1E6W.  
DR InterPro; IPR002198; ADH\_short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
KM Oxidoreductase; NAD; Mitochondrion.  
FT NP\_BIND 12 37 NAD (By SIMILARITY).  
FT ACT\_SITE 168 168 By SIMILARITY.  
SQ SEQUENCE 261 AA; 27140 MW; 8C7572B6A9A49780 CRC64;  
Query Match 91.7%; Score 1196; DB 1; Length 261;  
Best Local Similarity 91.6%; Pred. No. 1,2e-83;  
Matches 239; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

OY 1 MAACRSYKGLVAVITGGASGLGATARLVGGASAVLLDLPNSGGEPAQAKKIGNVVF 60  
DB 1 MAACRSYKGLVAVITGGASGLGATARLVGGASAVLLDLPNSDDETAQAKKIGKSCAF 60  
OY 61 APADYTSKDVQTLALAKKFGKGRVDVAVNCAGIAVASKTYNKKGGTHLEDFQRLDV 120  
DB 61 APADYTSKDVQALTLAKKFGKGRVDVAVNCAGIAVASKTYNKKSAHTLEDFQRYINV 120  
OY 121 NLMGTFNIRLVAGEMGNEDDGGQRCVITINTASVAEFEGVQQAAYSAKSGIVGMTL 180  
DB 121 NLIGTFNIRLVAGEMGNEDDGGQRCVITINTASVAEFEGVQQAAYSAKSGIVGMTL 180  
OY 181 PIARDLAPIGIRVMTIAPGLFGTPLTSLPERKCNFTLASQVPEPSRLGDPAEYAHVLQVAI 240  
DB 181 PIARDLAPIGIRVMTIAPGLFGTPLTSLPERKCNFTLASQVPEPSRLGDPAEYAHVLQVAI 240  
OY 241 ENPFLNGEVIRLDGAIKMP 261  
DB 241 ENPFLNGEVIRLDGAIKMP 261

RESULT 3  
HCD2\_RAT STANDARD; PRT; 260 AA.  
AC 070351; O9QYD4;  
DT 30-MAY-2000 (Rel. 39; Created)  
DT 30-MAY-2000 (Rel. 39; Last sequence update)  
DT 16-OCT-2001 (Rel. 40; Last annotation update)  
DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).  
GN HADH2 OR ERAB.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Gunn-Moore F.J., Tavaire J.M.;  
RT "Rattus norvegicus amyloid beta-peptide binding protein (ERAB) mRNA";  
RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RA Yang S.-Y., He X.-Y.;  
RT "Molecular cloning and characterization of the cDNA of rat brain short chain L-3-hydroxyacyl-CoA dehydrogenase";  
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
[3]  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RC TISSUE=Brain;  
RA MEDLINE=20481418; PubMed=11023795;  
RA Powell A.J., Read J.A., Banfield M.J., Gunn-Moore F., Yan S.D.,

"Recognition of structurally diverse substrates by type II 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding alcohol dehydrogenase (ABAD).";  
RT J. Mol. Biol. 303:311-327(2000).  
CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.  
CC -1- SUBUNIT: HOMOTETRAMER.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
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CC EMBL; AF049878; AAC05747.1; -  
DR EMBL; AF069770; AAF14653.1; -  
DR PDB; 1E3W; 25-MAY-01.  
DR PDB; 1E3S; 25-MAY-01.  
DR PDB; 1E6W; 25-MAY-01.  
DR InterPro; IPR002198; ADH\_short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
KM Oxidoreductase; NAD; Acetylation; 3D-structure.  
FT INIT\_MET 0 BY SIMILARITY.  
FT MOD\_RES 1 1 ACETYLATION (BY SIMILARITY).  
FT NP\_BIND 11 36 NAD (BY SIMILARITY).  
FT ACT\_SITE 167 167 BY SIMILARITY.  
FT CONFLICT 4 4 V -> C (IN REF. 2).  
SQ SEQUENCE 260 AA; 27114 MW; 30F7E72A95F9227 CRC64;  
Query Match 87.5%; Score 1141; DB 1; Length 260;  
Best Local Similarity 87.3%; Pred. No. 1,7e-79;  
Matches 227; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

OY 2 AAACRSYKGLVAVITGGASGLGATARLVGGASAVLLDLPNSGGEPAQAKKIGNVVF 61  
DB 1 AAACRSYKGLVAVITGGASGLGATARLVGGASAVLLDLPNSDETEKAKKIGKSCIF 60  
OY 62 PADYTSKDVQTLALAKKFGKGRVDVAVNCAGIAVASKTYNKKGGTHLEDFQRLDV 121  
DB 61 PANTSEKDVQALTLAKKFGKGRVDVAVNCAGIAVASKTYNKKGGTHLEDFQRYINV 120  
OY 122 LMGTFNIRLVAGEMGNEDDGGQRCVITINTASVAEFEGVQQAAYSAKSGIVGMTL 181  
DB 122 LMGTFNIRLVAGEMGNEDDGGQRCVITINTASVAEFEGVQQAAYSAKSGIVGMTL 180  
OY 121 NLIGTFNIRLVAGEMGNEDDGGQRCVITINTASVAEFEGVQQAAYSAKSGIVGMTL 180  
DB 182 IARDLAPIGIRVMTIAPGLFGTPLTSLPERKCNFTLASQVPEPSRLGDPAEYAHVLQVAI 241  
DB 181 IARDLAPIGIRVMTIAPGLFGTPLTSLPERKCNFTLASQVPEPSRLGDPAEYAHVLQVMT 240  
OY 242 ENPFLNGEVIRLDGAIKMP 261  
DB 241 ENPFLNGEVIRLDGAIKMP 260

RESULT 4  
HCD2\_MOUSE STANDARD; PRT; 261 AA.  
AC 008756;  
DT 15-JUL-1998 (Rel. 36; Created)  
DT 15-JUL-1998 (Rel. 36; Last sequence update)  
DT 15-JUN-2002 (Rel. 41; Last annotation update)  
DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).  
GN HADH2 OR HSD17B10 OR ERAB.

HCDD2\_HUMAN STANDARD; PRT; 261 AA.  
 ID HCDD2\_HUMAN  
 AC Q99714;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
 DE (Endoplasmic reticulum-associated amyloid beta-peptide binding  
 protein) (Short-chain type dehydrogenase/reductase XH96G2).  
 GN HADH2 OR ERAB OR XH96G2 OR SCHAD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCBI\_TaxID=9606;  
 RX MEDLINE=97476528; PubMed=9338779;  
 RA Yan S.D., Fu J., Soto C., Chen X., Zhu H., Al-Mohanna F.,  
 RA Collinson K., Zhu A., Stern E., Saldo T., Tohyama M., Ogawa S.,  
 RA Rober A., Stern D.;  
 RT "An intracellular protein that binds amyloid-beta peptide and  
 RT mediates neurotoxicity in Alzheimer's disease.";  
 RL Nature 389:689-695(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Zhuchenko O.P., Wehnert M., Bailey J., Sun Z.S., Lee C.C.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98337980; PubMed=9671743;  
 RA Miller A.P., Willard H.F.;  
 RT "Chromosomal basis of X chromosome inactivation: Identification of a  
 RT multigene domain in Xp11.21-p11.22 that escapes X inactivation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8709-8714(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Brain;  
 RX MEDLINE=98221216; PubMed=9553139;  
 RA He X.Y., Schulz H., Yang S.Y.;  
 RT "A human brain L-3-hydroxyacyl-coenzyme A dehydrogenase is identical  
 RT to an amyloid beta-peptide-binding protein involved in Alzheimer's  
 RT disease.";  
 RL J. Biol. Chem. 273:10741-10746(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Lung;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: BINDS INTRACELLULAR AMYLOID-BETA. BY INTERACTING WITH  
 CC AMYLOID-BETA. IT MAY CONTRIBUTE TO THE NEURONAL DYSFUNCTION  
 CC ASSOCIATED WITH ALZHEIMER DISEASE.  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL TISSUES BUT IS  
 CC OVEREXPRESSED IN NEURONS AFFECTED IN AD.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SCR) FAMILY.  
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DR EMBL: BC000372; AAH00372.1; -  
 DR HSSP: 070351; 1E3S.  
 DR Genew; HGNC:4600; HADH2.  
 DR MIM: 300256; -  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 KW Oxidoreductase, NAD.  
 FT NP\_BIND 12 37 NAD (BY SIMILARITY).  
 FT ACT\_SITE 168 168 BY SIMILARITY.  
 FT ACT\_SITE 168 168  
 SQ SEQUENCE 261 AA; 26923 MW; 9E74F242E3E6FEF1 CRC64;  
 Query Match 99.6%; Score 1299; DI 1; Length 261;  
 Best Local Similarity 99.6%; Pred. No. 1.9e-91;  
 Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MAAQRVYKGLVAIVTGGASGIGLATPARELVGQASAVLLDIPNSGGEAQAQKGNVVF 60  
 DB 1 MAAQRVYKGLVAIVTGGASGIGLATPARELVGQASAVLLDIPNSGGEAQAQKGNVVF 60  
 QY 61 APADTSEKVOFTALALAKGKFRGVDAVNCAGIVASKTYNLKKGOTHTEDFQRLDV 120  
 DB 61 APADTSEKVOFTALALAKGKFRGVDAVNCAGIVASKTYNLKKGOTHTEDFQRLDV 120  
 QY 121 NMGTFFNTRIVLAGENGQNEPDGQGVITNTASVAAPFGVGVQAAYSASKGIVGNTL 180  
 DB 121 NMGTFFNTRIVLAGENGQNEPDGQGVITNTASVAAPFGVGVQAAYSASKGIVGNTL 180  
 QY 122 NMGTFFNTRIVLAGENGQNEPDGQGVITNTASVAAPFGVGVQAAYSASKGIVGNTL 180  
 DB 122 NMGTFFNTRIVLAGENGQNEPDGQGVITNTASVAAPFGVGVQAAYSASKGIVGNTL 180  
 QY 181 PIARDLAPIGIRVMTAPLFGTLPILTSPEVCNFEIASQVPEPRLGPAPAYHLVQAI 240  
 DB 181 PIARDLAPIGIRVMTAPLFGTLPILTSPEVCNFEIASQVPEPRLGPAPAYHLVQAI 240  
 QY 241 IENPFLNGEIVIRLDGAIKMP 261  
 DB 241 IENPFLNGEIVIRLDGAIKMP 261  
 DB 241 IENPFLNGEIVIRLDGAIKMP 261  
 RESULT 2  
 HCDD2\_BOVIN STANDARD; PRT; 261 AA.  
 ID HCDD2\_BOVIN  
 AC 002691;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).  
 GN HADH2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NC NCBI\_TaxID=9913;  
 RX MEDLINE=97214648; PubMed=9061028;  
 RA Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.;  
 RT "Cloning and expression of cDNA for a newly identified isozyme of  
 RT bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into  
 RT mitochondria.";  
 RL Biochim. Biophys. Acta 1350:317-324(1997).  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SCR) FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial



Thu Jun 26 06:55:10 2003

us-09-931-186-6.rsp

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:47 ; Search time 7.8333 Seconds  
(without alignments)  
1381.956 Million cell updates/sec

Title: US-09-931-186-6  
Perfect score: 1304  
Sequence: 1 MAACRCVKGLVAVITGGAS.....ENFLNGEYTRLDGAIKMP 261

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1299	99.6	261	1	HCD2_HUMAN
2	1196	91.7	261	1	HCD2_BOVIN
3	1141	87.5	260	1	HCD2_RAT
4	1122	86.0	261	1	HCD2_MOUSE
5	913	70.0	255	1	HCD2_DROME
6	383.5	29.4	247	1	YD50_MYCTU
7	346	26.5	246	1	FABG_THENA
8	334	25.6	320	1	FABG_CUPLA
9	332.5	25.5	261	1	HDB8_HUMAN
10	328.5	25.2	244	1	FABG_VIBCH
11	313.5	24.0	247	1	FAGL_SYNY3
12	313.5	24.0	260	1	DHB8_MOUSE
13	309.5	23.7	246	1	FABG_BACSU
14	305	23.4	260	1	YK02_MYCTU
15	301	23.1	255	1	YWF0_BACSU
16	299	22.9	255	1	2BHD_STREX
17	294.5	22.6	548	1	YAVI_RHISN
18	293	22.5	249	1	BA71_EUBSP
19	291.5	22.4	244	1	FABG_VITRA
20	291.5	22.4	248	1	FABG_AQDNE
21	291	22.3	248	1	FABG_AQISP
22	289.5	22.2	244	1	FABG_ECOLI
23	289.5	22.2	256	1	Y019_THENA
24	288.5	22.1	246	1	FABG_ALCEU
25	284.5	21.8	248	1	FABG_CHLMU
26	284	21.8	259	1	CMTA_PSEPU
27	283.5	21.7	244	1	FABG_SALTY
28	282.5	21.7	246	1	NODG_AZOB
29	279.5	21.4	241	1	PHB8_ZOORA
30	279	21.4	246	1	PHB8_CHRYI
31	278	21.3	263	1	UCPA_SALTY
32	277	21.2	249	1	BA72_EUBSP
33	277	21.2	250	1	LINC_PSEPA

34	275.5	21.1	247	1	FABG_CHLIR
35	272.5	20.9	336	1	TS2_MALZE
36	272	20.9	250	1	LINC_PSEPA
37	272	20.9	251	1	Y325_THENA
38	272	20.9	319	1	FABG_ARATH
39	270.5	20.7	240	1	FAG2_SYNY3
40	270.5	20.7	241	1	PHB8_RHIME
41	269.5	20.7	261	1	DHXR_STRCM
42	268.5	20.6	262	1	DHGB_BACME
43	268.5	20.6	289	1	YHDF_BACSU
44	266.5	20.4	242	1	FABG_HAEIN
45	266.5	20.4	263	1	UCPA_ECO57
46	266	20.4	263	1	UCPA_ECOLI
47	261	20.0	261	1	DHGA_BACME
48	259	19.9	258	1	DH82_BACST
49	259	19.9	261	1	DH83_BACME
50	259	19.9	261	1	DH83_BACME
51	258	19.8	261	1	DH82_BACME
52	257.5	19.7	238	1	YOXD_BACST
53	257	19.7	247	1	FABG_MYCTU
54	257	19.7	256	1	BUDC_KLEPN
55	257	19.7	261	1	DH84_BACME
56	256	19.6	261	1	DH81_BACME
57	255.5	19.6	241	1	FABG_RICPR
58	254	19.5	261	1	DH8_BACSU
59	252.5	19.4	267	1	SORD_KLEPN
60	251.5	19.3	266	1	PGDH_HUMAN
61	249.5	19.3	245	1	NODG_RHIS3
62	246.5	18.9	258	1	BDEH_RHIME
63	246	18.9	253	1	Y4MP_RHISN
64	245	18.8	235	1	YV06_PSEAE
65	245	18.8	253	1	GNO_GLUOX
66	244.5	18.8	256	1	3BHD_COMTE
67	244.5	18.8	262	1	YXBG_BACST
68	243	18.6	270	1	DHMA_FIAS1
69	242.5	18.6	261	1	ACT3_STRCO
70	242.5	18.6	261	1	YCGW_ECOLI
71	242	18.6	248	1	FABG_CHLIR
72	240.5	18.4	285	1	YHXC_BACSU
73	239	18.3	255	1	HDHA_ECOLI
74	238	18.3	247	1	FABG_PSEAE
75	235	18.0	257	1	YXRF_BACSU
76	234.5	18.0	245	1	NODG_RHIME
77	232.5	17.8	258	1	BDEH_ALCEU
78	231.5	17.8	273	1	TRN1_DANST
79	231	17.7	255	1	FABG_MYCAV
80	229	17.6	894	1	FOX2_NEUCR
81	226.5	17.4	242	1	PHAB_PARDE
82	224.5	17.2	249	1	DH82_STRVN
83	224.5	17.2	256	1	DH80_RHOSH
84	224	17.2	254	1	IDNO_ECOLI
85	223.5	17.1	241	1	BUDC_KLEFE
86	223.5	17.1	272	1	DH81_STRVN
87	223.5	17.1	900	1	FOX2_YEAST
88	220.5	16.9	259	1	SRID_ECOLI
89	218	16.9	254	1	KDUD_BACSU
90	217.5	16.7	253	1	KDUD_ECOLI
91	217	16.6	248	1	Y452_LISIN
92	215	16.5	242	1	FABG_ACTAM
93	215	16.5	255	1	FABG_MYCSM
94	213	16.3	144	1	DH88_CALJA
95	213	16.3	268	1	TRN1_DASTO
96	212.5	16.3	268	1	Y432_LISMO
97	212.5	16.3	256	1	MTDH_UROFA
98	212	16.3	281	1	PHB8_COMTE
99	212	16.3	299	1	YHXD_BACSU
100	211.5	16.2	278	1	Y4LA_RHISN

ALIGNMENTS

P38004	chlamydia t
P50160	zea mays (m
P50198	pseudomonas
Q9wy90	thermotoga
P33207	arabidopsis
P73826	synechocyst
P50205	rhizobium m
P41177	streptomyces
P07999	bacillus me
O07575	bacillus su
P43713	haemophilus
Q8xbj4	escherichia
P37440	escherichia
P10528	bacillus me
P80869	bacillus su
P39484	bacillus me
P40288	bacillus me
P39483	bacillus me
P14802	bacillus su
Q48930	mycobacteri
Q48436	klebsiella
P39485	bacillus me
P39482	bacillus me
P30941	ricketsia
P12310	bacillus su
P37079	klebsiella
P15428	homo sapien
P72332	rhizobium s
O86034	homo sapien
P55575	rhizobium s
O51576	pseudomonas
P50199	gluconobact
P19871	comamonas t
P46331	bacillus su
P22441	flavobacter
P16544	streptomyces
P76633	escherichia
Q928P2	chlamydia p
P40397	bacillus su
P25529	escherichia
O54438	pseudomonas
P42314	bacillus su
P06234	rhizobium m
O9x6u2	alcaligenes
O07399	mycobacteri
O01373	neurospora
P50304	paracoccus
P16543	streptomyces
O59787	rhodobacter
P39345	escherichia
O04520	klebsiella
P16542	streptomyces
Q02207	saccharomyces
P05707	escherichia
P50842	bacillus su
P37769	escherichia
Q92867	escherichia
P17072	actinobacteri
P71554	mycobacteri
O9gm33	callitrix
P50145	datura stra
P25145	listeria mo
O00058	uroyuncus fa
O46303	c cis-2,3-d
P40388	bacillus su
P55541	rhizobium s



DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)  
 DE 3-oxoacyl-[acyl-carrier protein] reductase.  
 GN FABG OR ALR1894.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 RT cyanobacterium Anabaena sp. strain PCC 7120.";  
 RL DNA Res. 8:205-213(2001).  
 DR EMBL; AP003587; BAB73593.1; -;  
 DR InterPro; IPR002198; ADH\_short.  
 DR InterPro; IPR01092; HLH\_Basic.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR PROSITE; PS00038; HELIX\_LOOP\_HELIX; UNKNOWN\_1.  
 KM Complete proteome.  
 SQ SEQUENCE 251 AA; 26218 MW; 57D0712F8EA6B698 CRC64;  
  
 Query Match 25.7%; Score 334.5; DB 16; Length 251;  
 Best Local Similarity 33.1%; Pred. No. 2.6e-15;  
 Matches 91; Conservative 46; Mismatches 97; Indels 41; Gaps 7;  
  
 QY 1 MAACRSYKGLVAVITGASGLGATARLVGQASA-----VLDLPNSGG 47  
 DB 1 MAISENLRGQVAVVTGASRGIGRAIALELANLGATVYVNYASSSTADEVVAEITGAGG 60  
 QY 48 EAQAKKLGNNVVFAPADVTSEKDVQFALALAKGKFRVDVAVNCAGIYAVASKTYNLKKG 107  
 DB 61 EAVALK-----ADVSQVEQYDNLNGAIDKFRIDILYNNAGITRDITLLRMKP-- 109  
 QY 108 THLEDFQRLVDVNLMGTFENVIRLVAGEMGQNEPDGQGGVITNTASVAAFESQVQAA 167  
 DB 110 ----EDMQAVIDLNTGVLCTRAVSKMLKQ-----RSGRIINITSVAGOMGNPGQAN 159  
 QY 168 YSASKGIIVGWTLPFARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPSPRL 227  
 DB 160 YSAKAGYIGFTKYAKELASRGITVAVNAVAPFTAITDXTSLKSE---GIQYIPL-GRY 215  
 QY 228 GDPAEYAHVQAIIENP--FLNGEVIRLDGAIRM 259  
 DB 216 GQPEIAGVRFLLADPAAYITGQVFNVGDGMVM 250

Search completed: June 23, 2003, 14:32:45  
 Job time : 32.6667 secs

Query Match 26.1%; Score 340.5; DB 3; Length 297;  
 Best Local Similarity 32.0%; Pred. No. 1.3e-15;  
 Matches 98; Conservative 39; Mismatches 102; Indels 67; Gaps 8;

QY 6 RSVYGLVAVITGASGLATAEELVVGOGASAVILDPNS-----GGEAQ 50  
 DB 2 RSLLEKQALITGGSGIGLAIARLYLEGSVTLTGTESTLORASQSLLSPLHSPAQ 61  
 QY 51 AKRLGNVVFAPAVTSEKDVQTL-ALAKGEGRVAVNACAGIAVAS--KTYNLKG 106  
 DB 62 QPSDTKRVSYHPLAVTASSMEDLLQNSNGKGRVDILNCAGITGRSPLMT----- 115  
 QY 107 QTHLEDFORVLDVNLKGTENVIRLVAGENGNEP-----DQCG----- 145  
 DB 116 ---SIEVEGILLDYNLRTYLGCKFVRAMLRNPSOQHPVRKADEGAGVEGTEEG 172  
 QY 146 -----QRGVINTASVAAFEVGOVGOAASASKGIVGKTLPIARDLAPIGI 191  
 DB 173 KGEKGGCVRGVREGVITIVASLAKGVIGTSVAAKAGVYGLITSLAHYGRSGI 232  
 QY 192 RVMTIAPGLFETPLITSIPKVCNFTLASQVFPFSLDDPAEYAHVQATIEENPLNGEVI 251  
 DB 233 RVNAVLPQYIETDMTTGKKNP---SILQIPL-GRFGTDEVADALFLIKNPYANNCVL 288  
 QY 252 RLDDGI 257  
 DB 289 NLDGCL 294

RESULT 23  
 Q8R9W0 PRELIMINARY; PRT; 247 AA.

AC 08R9W0  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Dehydrogenases with different specificities (related to short-chain  
 DE alcohol dehydrogenases).  
 GN FASG3 OR TTE1472.  
 OS Thermoaerobacter tengcongensis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
 OC Thermoaerobacteriales; Thermoaerobacteriaceae; Thermoaerobacter.  
 OC NCBI\_TaxID=119072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MBAT / JCM11007;  
 RX MEDLINE=21992816; PubMed=11997336;  
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;  
 RT "A complete sequence of T. tengcongensis genome.";  
 RL Genome Res. 12:689-700(2002).  
 DR EMBL, AF013105; AAM24694.1; -.  
 KW Complete proteome.  
 SQ SEQUENCE 247 AA; 26606 MW; 357D82B8C60E7947 CRC64;

Query Match 25.9%; Score 337.5; DB 16; Length 247;  
 Best Local Similarity 34.3%; Pred. No. 1.6e-15;  
 Matches 87; Conservative 48; Mismatches 100; Indels 19; Gaps 6;

QY 12 VAVITGASGLATAEELVVGOGASAVILDPN--SGGEA--QAKKLGNNVVFAPAVTS 67  
 DB 7 VAVITGASGLATAEELVVGOGASAVILDPN--SGGEA--QAKKLGNNVVFAPAVTS 67  
 QY 68 EKDVTALALAKGFRGVAVNACAGIAVASKTYNLKKGQTHLEDFORVLDVNLKGTEN 127  
 DB 67 YHEVEKAVERKYLEEGSIDVYVNNAGITKMLILKMEB-----EEMDQVLDVNLKGAFN 120  
 QY 128 VIRLVAGENGNEPDDGGGVINTASVAAFEVGOVGOAASASKGIVGKTLPIARDIA 187  
 DB 121 VIKPSAKMIKK-----RKGIINTISSVGLMGVNGVGOAANASAKAGITIGTKSVAKELA 174  
 QY 188 PIGIRVMTIAPGLFETPLITSIPKVCNFTLASQVFPFSLDDPAEYAHVQ--AIENPF 245

DB 175 SRITVNAVAPGIEITDMTNVLKEDIKEMAKSIPL-KRAGKPEEVAEYVAFIASSASDY 233  
 QY 246 LINGEYRLDGAIRM 259  
 DB 234 ITGQVINVDSGMV 247

RESULT 24  
 Q9K636 PRELIMINARY; PRT; 246 AA.

AC 09K636  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE 3-oxoacyl-(acyl-carrier protein) reductase.  
 GN BH3896.  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Bacillaceae; Bacillus.  
 OC NCBI\_TaxID=86655;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C-125 / JCM 9153;  
 RX MEDLINE=20512582; PubMed=11058132;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fujii F., Hiramata C., Nakamura Y., Ogasawara N., Kuhara S.,  
 RA Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC EMBL, AP001520; BAB07615.1; -.  
 DR HSSP; P19992; IHDC.  
 DR InterPro; IPR002196; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; UNKNOWN\_1.  
 KW Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 246 AA; 25357 MW; 7CEAB2C4EB155376 CRC64;

Query Match 25.7%; Score 335; DB 16; Length 246;  
 Best Local Similarity 34.6%; Pred. No. 2.4e-15;  
 Matches 92; Conservative 40; Mismatches 94; Indels 40; Gaps 8;

QY 8 VKGLVAVITGASGLATAEELVVGOGASAVILDPN--SGGEA--QAKKLGNNVVFAPAVTS 67  
 DB 3 LNKVNAITGAGGIGATRAKFAKREGAKYIVCDVAEEVAKTYVALIQGGGGA-----LG 58  
 QY 56 NNVVFAPADVTSEKDVQTLALAKGFRGVAVNACAGIAVASKTYNLKKGQTHLEDFQ 115  
 DB 59 SVV-----DVTQRKDYKVNINQVIERFETLDVYVNNAGITADQLTNMTDAQ-----WD 107  
 QY 116 RVLVDVNLKGTENVIRLVAGENGNEPDDGGGVINTASVAAFEVGOVGOAASASKGIGI 175  
 DB 108 DVIDVNLKGTENVIRLVAGENGNEPDDGGGVINTASVAAFEVGOVGOAASASKGIGI 175  
 QY 176 VGNLPIARDLAPIGIRVMTIAPGLFETPLITSIPKVCNFTLASQVFPFSLDDPAE--- 232  
 DB 162 NGMTKTAKEKLGYNIRVNNAVAPGILITPTKPEKVLKVMKEAVL--NRLGTVEEVAN 220  
 QY 233 -YAHVQATIEENPLNGEYRLDGI 257  
 DB 221 GYAFV--ASDEASFTIGTITADGV 244

RESULT 25  
 Q8YVTO PRELIMINARY; PRT; 251 AA.

AC 08YVTO  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 15692 / PAOI;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
 RA Brody L.A., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RA "Complete genome sequence of *Pseudomonas aeruginosa* PAOI, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 (SDR) FAMILY.  
 CC EMBL; AF004854; AAC07777.1; -  
 DR HSSP; P50163; 2AE1.  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.  
 DR OXIDOREDUCTASE; Complete proteome.  
 KW OXIDOREDUCTASE; Complete proteome.  
 SQ SEQUENCE 252 AA; 26720 MW; FIF445AB82C2DBDE CRC64;

Query Match 27.2%; Score 355; DB 16; Length 252;  
 Best Local Similarity 35.1%; Pred. No. 1.1e-16;  
 Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;  
 QY 8 VKGIIVAVITGASGIGLTAERLVGGASAVLDPN-----SGGEQAARKLG 55  
 DB 3 LKDKVITITGGGGGRAMGETLNGKGRKLVLDNRELRDEAVAAKAGGDRRA---- 58  
 QY 56 NNVPAPADVTSEKVDQTLALAKGKGRVDVAVNCAGIAVASKTYLKKGQTH-TLED 113  
 DB 59 -----YVCNVADEQVTHMVAQVASFAGANGLVNAGILRDGLTIKVKDQLSKMSLAQ 113  
 QY 114 FQRTVDVNLGTFENIRIVAGEMQ--NEPDGQGRGVIINTASVAEFEGVGAAYASAS 171  
 DB 114 WQSVTDVNLGTFELCTREVAAMTELKNE-----GAVITSSISR AGNMGASAPSA 165  
 QY 172 KGIIVGMLPIARDAPIGIRMTAPGLFTPLTSLPERVCNFLASQVFPSPRLGPPA 231  
 DB 166 KAGVAADTVYMAKELARIGIRVAGVAPGFIEEMTAGKPPALEKMTGIPPL-KRMGPV 224  
 QY 232 EYAHVQAIITENPFLNGEVIRLDGAIIM 259  
 DB 225 ETASHVAYITENDYITGRVLELDGGLRL 252

## RESULT 21

Q97DA6 PRELIMINARY; PRT; 249 AA.

ID 097DA6  
 AC 097DA6; 01-OCT-2001 (TREMblrel. 18, Created)  
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE 3-oxoacyl-acyl carrier protein reductase.  
 GN CAC3574.  
 OS Clostridium acetobutylicum.  
 OC Bacteria: Firmicutes: Bacillus/Clostridium group: Clostridia:  
 OC Clostridiales: Clostridiaceae; Clostridium.  
 RX MEDLINE=1465286;  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,  
 RA Tatusov R.L., Sabetie F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RA "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium *Clostridium acetobutylicum*.";  
 RL J. Bacteriol. 183:4823-4838(2001).

DR EMBL; AF007854; AAK81497.1; -  
 DR InterPro; IPR002198; ADH\_short.  
 DR InterPro; IPR001092; HLH\_basic.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR PROSITE; PS00038; HELIX\_LOOP\_HELIX; UNKNOWN\_1.  
 KW Complete proteome.  
 SQ SEQUENCE 249 AA; 26247 MW; B13D7EDAC1A626A CRC64;

Query Match 26.3%; Score 343.5; DB 16; Length 249;  
 Best Local Similarity 33.2%; Pred. No. 6.3e-16;  
 Matches 86; Conservative 56; Mismatches 96; Indels 21; Gaps 6;  
 QY 8 VKGIIVAVITGASGIGLTAERLVGGASAVLDPN-----AKRLGNVPAP 62  
 DB 5 LSGKVAVITGAGRGRLALALAAEGANLV-VNTRSSAEETQKLEIEELGSAVAVK 63  
 QY 63 ADVTSEKVDQTLALAKGKGRVDVAVNCAGIAVASKTYLKKGQTHLEDFQRLVNL 122  
 DB 64 ADISKYDEAEITIKKALDEYGVTDIVNNAGITKDLNLRKE-----EDFDSVINVL 117  
 QY 123 MGFENIRLVAGMGNEPDGQGRGVIINTASVAEFEGVGAAYASASKGIVGMLPI 182  
 DB 118 KGAFNCKIKHTSRVMLK-----KSGKITISSVIGLIGNAQVYMAAKAGIIMTSV 171  
 QY 183 ARDLAPIGIRVMTAPGLFTPLTSLPERVCNFLASQVFPSPRLGPPAEVAHVOAITE 242  
 DB 172 AKELASRGITVNVNAGIISKDMDALTDKORESIIVAAVPL-NKVGAEADVAVNLVFLAS 230  
 QY 243 --NPLNGEYIRLDGAIIM 259  
 DB 231 DLSSYITGVINVDGGMV 249

## RESULT 22

Q42774 PRELIMINARY; PRT; 297 AA.

ID 042774  
 AC 042774; 01-JUN-1998 (TREMblrel. 06, Created)  
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE 3-oxoacyl-[acyl-carrier-protein]-reductase.  
 GN OAR-1 OR B2A19.180.  
 OS Neurospora crassa.  
 OC Eukaryota: Fungi: Ascomycota: Pezizomycotina: Sordariomycetes:  
 OC Sordariiales: Sordariaceae; Neurospora.  
 RX MEDLINE=5141;  
 RA Buerger F., Brors B., Welts H.;  
 RA submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Schulte U., Algn V., Hohnsels J., Brandt P., Fartmann B., Holland R.,  
 RA Nyakatura G., Kewes H.W., Mannhaupt G.;  
 RA submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA German Neurospora genome project;  
 RL submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 (SDR) FAMILY.  
 CC EMBL; AF042860; AAB9799.1; -  
 DR EMBL; AL330092; CAB98248.1; -  
 DR HSSP; O70351; 1B6W.  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR OXIDOREDUCTASE.  
 KW OXIDOREDUCTASE.  
 SQ SEQUENCE 297 AA; 31342 MW; 8DC08FEDF564196F CRC64;

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DB 8 AVITGKXKRRAGRPARRRRL----ARSALFDLNDKGAANAVALGADKAREYNNVS 63
OY 67 SEKVQYALALAKGKFRGVDAVAVNCAGIAVASKTYNNLKGGTHLEDFQRYLDVNLGTF 126
DB 64 DEAVTAIDQAHDFLGLGNVAMNCAGILGAGRV--LKEGPMPLAGFGQYVNVNLVGSF 121
OY 127 NVIRLVAGMGONPEPDGCGRGVITINTASVAFEGVQAAVSASKGIVGMLPIARDL 186
DB 122 NVAAANAARMQHNENGTGEGVITINTASIAIEGQIGQAAVYASKGIVGMLPIAREL 181
OY 187 APIGIRVMTIAPGLGFTPLTSLPEKV 213
DB 182 SRFGIRVMTIAPGVFWTMDVGMPEAV 208

RESULT 18
OQXHL1 PRELIMINARY; PRT; 246 AA.
AC 08XHL1;
DR 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE 3-oxoacyl-lacyl-carrier-protein] reductase.
GN FABG OR CPE1070.
ON Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ogasawara K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hatiori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL: AP003189; BAB80776.1;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Complete proteome.
SQ SEQUENCE 246 AA; 26267 MW; CD90B8C650EC817 CRC64;

Query Match 29.0%; Score 378.5; DB 16; Length 246;
Best Local Similarity 36.2%; Pred. No. 2,6e-18;
Matches 94; Conservative 47; Mismatches 96; Indels 23; Gaps 7;
```

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AC 099YD6;
DR 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Putative beta-ketacyl-ACP reductase (EC 1.1.1.100).
GN FABG OR SPY1749.
ON Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SE370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian X., Clifton S.W., Roe B.A., McLaughlin R., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R., Ren Q., Zhu H., Song L., White J.,
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC 1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(CDR) FAMILY.
DR EMBL: AE006603; AAK34493.1;
DR HSP: P50162; IAE1.
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR01092; HLH_basic.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR01608; BACINVASINC.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 244 AA; 26002 MW; 67EC23870D40D65 CRC64;

Query Match 27.6%; Score 360.5; DB 16; Length 244;
Best Local Similarity 35.8%; Pred. No. 4,3e-17;
Matches 93; Conservative 41; Mismatches 101; Indels 25; Gaps 5;

OY 8 VKGLAVITGASGLATAERLVGGASAVLLDLPNSGGEAQAOKL-----GNVYF 60
DB 3 IKGNIFITGTRIGIAMAHQFASLSANIVL-----NGSAISEELVAFSTDYGVTVT 57
OY 61 APADVTSEKDVQYALALAKGKFRGVDAVAVNCAGIAVASKTYNNLKGGTHLEDFQRYLDV 120
DB 58 ISGVSESEAKRVVNEAIESLSIDVYNNAGIT-----NDKLMKMEDEDERVLKI 111
OY 121 NLMGTFVIRLVAGMGONPEPDGCGVITINTASVAFEGVQAAVSASKGIVGML 180
DB 112 NLGAFNNTQSVL-----KPIKARQAGALINSSVGLTGNIQAVYASKAGMIGFTK 165
OY 181 PIARDLAPIGIRVMTIAPGLGFTPLTSLPEKVCNFIASGVPPPSRLGDPAEYAHLYQAI 240
DB 166 SVAREVAVARNICVANAIAAGFIESDMTGVLPKMQEQLISQIPM-KRIGKQGEVAHLASFL 224
OY 241 IENPLNGEVTIRLDGALRMQ 260
DB 225 VEODYITGQVTAIDGGMTO 244

RESULT 20
OQ9HW15 PRELIMINARY; PRT; 252 AA.
AC 09HW15;
DR 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, last annotation update)
DE Probable short-chain dehydrogenase.
GN PA4389.
ON Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
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[illegible]

QY	254	DGAIRM	259
Db	247	DGALRM	252
RESULT	13		
Q80F12	Q80F12	PRELIMINARY;	PRT; 257 AA.
AC	Q80F12;		
DT	01-JUN-2002	(TREMBLrel. 21, Created)	
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)	
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)	
DE	3-hydroxacyl-CoA dehydrogenase type II.		
GN	Atv1415 OR AGR_C.2613.		
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).		
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;		
OC	Rhizobiaceae; Rhizobium.		
OX	NCBI_TaxID=176299;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21608550; PubMed=11743193;		
RA	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,		
RA	Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Moo L.,		
RA	Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. St.,		
RA	Chapman P., Glendinning J., Deatherage G., Gillet W., Grant C.,		
RA	Kuyavayn T., Levy R., Li M.-J., McCelland E., Palmieri A.,		
RA	Raymond C., Rouse G., Seshimachak C., Wu Z., Romero P., Gordon D.,		
RA	Zhang S., Yoo H., Tao Y., Bidale P., Jung M., Krespan W., Perry M.,		
RA	Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,		
RA	Chumley F., Tingey S.V., Tomp J.F., Gordon M.P., Olson M.V.,		
RA	Nester E.W.;		
RT	"The genome of the natural genetic engineer Agrobacterium tumefaciens		
RT	C58.";		
RL	Science 294:2317-2323(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21608551; PubMed=11743194;		
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,		
RA	Quirillo B., Goldman B.S., Cao Y., Ashkenai M., Halling C., Mallin L.,		
RA	Hounlet K., Gordon J., Vaudin M., Iatichoux O., Epp A., Liu F.,		
RA	Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Martelz B.,		
RA	Flanagan C., Crowell C., Gursun V., Lomo C., Sear C., Strub G.,		
RA	Cleto R., Slater S.;		
RT	"Genome sequence of the plant pathogen and biotechnology agent		
RT	Agrobacterium tumefaciens C58.";		
RL	Science 294:2323-2328(2001).		
DR	EMBL; AE009102; AAL42421.1;		
DR	EMBL; AE008067; AAK87207.1;		
KW	Complete proteome.		
SC	SEQUENCE 257 AA; 26622 MW; FF74A61FEC4B2B5C CRC64;		
Query Match	49.2%;	Score 642;	DB 16; Length 257;
Best Local Similarity	51.7%;	Pred. No. 3 6e-36;	
Matches 134;	Conservative 41;	Mismatches 76;	Indels 8; Gaps 3
QY	7 SVKGLVAVITGGASGIGLTAERLVYOGGASAVLLDLPNSGGEAOAKKIGNNVFAFADVT	66	
Db	2 NTEGAGALVITGGAAGVAVEMTLARGAAYVITFDENGEGAKKLAIEIGKAV--OGDVT	59	
QY	67 SEKDVTALALAKKRGKRGVAVVNOAGIVASKTYLKKGGVHTLEDDPQVLDVNLKMGF	126	
Db	60 SDADKQALATKYVASAKAGKIRILVNCAGISTAGRI--LGRGGPQPLADFDQVLRKVNLTGTF	117	
QY	127 NVIRLVAGEGONEPDG---GORGVIINTASVAAFEGQVQOAMYSASKSGIVGNTLPT	182	
Db	118 NMRRLAAHMAERREDEGGDSRODNQVIVNFTASVAFEQIGQAAAYAAASKGIVSLALPA	177	
QY	183 ASDLAPIGRVMTIAPGFGFTLLSLPKYCNFLASQVFPFRRIGDDPREVAHVNAAITE	242	
Db	178 ARELAERIRVNTVAAGITFLTPLOGGLPEOVGDSILAGQIPHSRLDDPPEAFATVFFLIE	237	

QY	243	NPNGEVRITLGAIRMP	261
DB	238	NDYANGEVIRLDGAIRMP	256

RESULT 14

09DCX5

ID 09DCX5 PRELIMINARY: PRT: 126 AA.

AC 01-JUN-2001 (TEMPBLREL, 17, Created)

DT 01-JUN-2001 (TEMPBLREL, 17, Last sequence update)

DT 01-JUN-2002 (TEMPBLREL, 21, Last annotation update)

DE Hydroxyacyl-coenzyme A dehydrogenase, type II.

GN HSD17B10 OR HADH2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxId:10090;

[1]

SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=KIDNEY;

RX MEDLINE=21085660; Pubmed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S., Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Castavet T., Fleischmann W., Gaasterland T., Gissi C., King B., Kikuchi H., Kuchel P., Lewis S., Matsuo Y., Nishida I., Pesole G., Quackenbush J., Schiraldi L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Bonfieldi D., Bojunga N., Carninci P., de Bonard M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Guelincich S., Hill D., Hofman M., Hume D.A., Kaniya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S., Hayashizaki Y.

RA \*Functional annotation of a full-length mouse cDNA collection.\*;

RL Nature 409:685-690(2001)

CC -I- STIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

CC HBSL; AK002368; BAB2204.1; -

DR EMBL; O70351.1; E6W.

DR MGP; MGI:1333871; Hsdl7b10.

DR InterPro: IPR002198; ADH\_short.

DR Pfam; PF00106; adh\_short.1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH\_SHORT; 1.

KM Oxidoreductase.

SEQ SEQUENCE 126 AA; 13265 MW; 78FPB6D441B9989D CRC64;

QY Query Match 46.5%; Score 607; DB 11; Length 126;

DB Best Local Similarity 95.2%; Pred No. 3.7e-34;

DB Matches 120; Conservative 2; Mismatches 4; Indels 0; Gaps 0

QY 136 MGONEPDGQGRVVIINTASVAFAEGQVQAASAKSGIVGMLPIARDIAPIGIRVMT 195S

DB 1 MGONEPDGQGRVVIINTASVAFAEGQVQAASAKSGIVGMLPIARDIAPIGIRVMT 60

QY 196 IAPLFTPLTLLSPKVCNGLASQVPPSRIGDAEVAHLYQATLENPFINGEVIRLDG 255S

DB 61 IAPLFTPLTLLSPKVCNGLASQVPPSRIGDAEVAHLYQATLENPFINGEVIRLDG 120S

QY 256 AIRMP 261

DB 121 AIRMP 126

RESULT 15



OX NCBI\_TaxID=305;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GM1000;  
 RX MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Manganot S.,  
 RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,  
 RA Chandler M., Christine N., Claudel-Renard C., Cunne S., Demange N.,  
 RA Gaupin C., Lavie W., Moisan A., Robert C., Sarrin W., Schlex T.,  
 RA Sigler P., Theault P., Whalen M., Winkler P., Levy M.,  
 RA Weissenbach J., Boucher C.A.;  
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";  
 RL Nature 415:497-502(2002).  
 DR EMBL: AL646070; CABD6241.1;  
 RL InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Oxidoreductase; Complete proteome.  
 KW SEQUENCE 252 AA; 25642 MM; DBEBCDA99179DF CRC64;

Query March 57.9%; Score 689.5; DB 16; Length 252;  
 Best Local Similarity 57.1%; Pred. No. 2.1e-39;  
 Matches 145; Conservative 33; Mismatches 71; Indels 5; Gaps 3;

QY 8 VKGLVAVITGASGSLGATTAERLVGOGASAVLLDLPNSGGEQAQKLGNNVFPADYTS 67  
 DB 3 IRDQVFYITGASGSLGATTAERLVGOGASAVLLDLPNSGGEQAQKLGNNVFPADYTS 60  
 QY 68 EKDVOITALAKKGFGRVDVAVNCAGIAVASKTYNLKKGQHTLEDQFVLDVNLGTEN 127  
 DB 61 EADGQAAVQAAAT-SLGLAGLVNCGIAPASRT--VGLAGHPILDQFAPVNLIGTEN 117  
 QY 128 VIRLVAGEKQNEPDGQGVIIINTASVAEFGQVQAAVSAKSGIVGNTLPARDIA 187  
 DB 118 MIRLAATMTANAPRAGESEVVIINTASVAEFGQVQAAVSAKSGIVGNTLPARDIA 177  
 QY 188 PIGIRVMTIAPGLFGLTSLPERVCNFLASQVPPFSRLDPAEYAHVQALTEENPFLN 247  
 DB 178 RDGIRVMTIAPGLFGLTSLPERVCNFLASQVPPFSRLDPAEYAHVQALTEENPFLN 237  
 QY 248 GEVIRLDGAIKMP 261  
 DB 238 GETIRLDGAIKMP 251

RESULT 9  
 Q92YSL PRELIMINARY; PRT; 255 AA.  
 AC Q92YSL;  
 DT 01-DEC-2001 (TREMREL. 19, Created)  
 DT 01-DEC-2001 (TREMREL. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMREL. 20, Last annotation update)  
 DE Probable.  
 GN RA0792 OR SMA1452.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Plasmid pSymba (megaplasmid 1).  
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 CC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396509; PubMed=11481432;  
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,  
 RA Barclay-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,  
 RA Gurial M., Hong A., Hultar L., Hyman R.W., Kahn D., Kahn M.L.,  
 RA Kallan S., Keating D.H., Palm C., Peck W.C., Strzycki R., Wells D.H.,  
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;  
 RT "Nucleotide sequence and predicted functions of the entire  
 RT Sinorhizobium meliloti pSymba megaplasmid.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).  
 DR EMBL: AE007266; AAK65450.1; -

DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PROSITE: PS00061; ADH\_SHORT; UNKNOWN\_1.  
 KW Plasmid; Complete proteome.  
 SQ SEQUENCE 255 AA; 26329 MM; EDC7942D3ED867C CRC64;

Query March 51.8%; Score 675; DB 16; Length 255;  
 Best Local Similarity 55.1%; Pred. No. 2e-38;  
 Matches 140; Conservative 34; Mismatches 78; Indels 2; Gaps 1;

QY 8 VKGLVAVITGASGSLGATTAERLVGOGASAVLLDLPNSGGEQAQKLGNNVFPADYTS 67  
 DB 3 LKSRVYITGASGSLGATTAERLVGOGASAVLLDLPNSGGEQAQKLGNNVFPADYTS 62  
 QY 68 EKDVOITALAKKGFGRVDVAVNCAGIAVASKTYNLKKGQHTLEDQFVLDVNLGTEN 127  
 DB 63 EADATALLAPAKQEFHVGILVNCAGTARKEI--LGRGPHALDSFATVAVNLIGTEN 120  
 QY 128 VIRLVAGEKQNEPDGQGVIIINTASVAEFGQVQAAVSAKSGIVGNTLPARDIA 187  
 DB 121 MIRLAETVMSQGPDPDAGRGVIVNTASIAAFDQIGQAAVSAKSGIVGNTLPAREIA 180  
 QY 188 PIGIRVMTIAPGLFGLTSLPERVCNFLASQVPPFSRLDPAEYAHVQALTEENPFLN 247  
 DB 181 RFGIRVMTIAPGLFGLTSLPERVCNFLASQVPPFSRLDPAEYAHVQALTEENPFLN 240  
 QY 248 GEVIRLDGAIKMP 261  
 DB 241 GEVIRLDGAIKMP 254

RESULT 10  
 Q006544 PRELIMINARY; PRT; 250 AA.  
 AC Q006544;  
 DT 01-JUN-1997 (TREMREL. 04, Created)  
 DT 01-JUN-1997 (TREMREL. 04, Last sequence update)  
 DT 01-MAR-2002 (TREMREL. 20, Last annotation update)  
 DE Oxidoreductase, short-chain dehydrogenase/reductase family.  
 GN RV1144 OR MTC165.11 OR MTC1177.  
 GN Mycobacterium tuberculosis.  
 OS Mycobacterium tuberculosis.  
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 CC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Whitehead B.G.;  
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / OSHKOSH;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Hatt D., Hickey E.,  
 RA Kjolnery J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishel W.;  
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and  
 RT laboratory strains.";  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z95984; CAB09032.1; -  
 DR EMBL: AE006996; AAK45436.1; -  
 DR HSSP: O70351; IE3S.



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OY 123 MGFENVRLVAGEMGNEPDGQGVYINTASVAFAEGVGQAAYSASKSGITVMTLP1 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 120 LGTFNVIRHGVALLMGEHHEKDNKNGRGVYINTASVAADGQGTGASASKGAIVGMLPL 179
OY 183 ARDIAPGIRVMTIAPGLFGPILTLSPKVCNPLASQVPPPSRLGDPAEYAHVQAIIIE 242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 180 ARDEAGGIRVMTIAPGLMDPILTLSPKVCNPLASQVPPPSRLGDPAEYAHVQAIIIE 239
OY 243 NPFLNGEYIRLDGAIIM 259
    | ||| | ||| | ||| |
DB 240 NQYNGEYIRLDGAIIM 256
```

## RESULT 6

```
O910T0 PRELIMINARY; PRT; 255 AA.
AC O910T0:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Probable short-chain dehydrogenase.
GN PA2554.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
OY NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westhick-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Iarsh K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
    (SDR) FAMILY.
DB EMBL: AE004683; AAC05942.1; -
DR HSP: 070351; IBS3.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Oxidoreductase: Complete proteome.
SQ SEQUENCE 255 AA; 26426 MW; EB8FF28712D2936D CRC64;
```

```
Query Match 55.2%; Score 720; DB 16; Length 255;
Best Local Similarity 57.5%; Pred. No. 1.8e-41;
Matches 145; Conservative 39; Mismatches 66; Indels 2; Gaps 1;

OY 8 VKGLAVITGGASGLATAEIRLVGGASAVLLDLPNSGGEAOKKLGNNVFAADYVS 67
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3 IENKRVLTGSSSGSLGATKALVBOGSKVTLADINAEAGAKAEELGAKRFRAIDIAS 62
OY 68 EKDVOTALAKKGRFGRVAVNCAIGIAVASKTYNLKKGQTHLTEDFORVLDVNLGTFN 127
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 63 EADGRQAAVAALAEAFGGHGLANCAGVAPAEKV--LGRNGIHAILESFRVIDIMLVGSFN 120
OY 128 VIRLVAGEMGNEPDGQGVYINTASVAFAEGVGQAAYSASKSGITVMTLP1ARDIA 187
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 MRLIAEAMKSNPQGGEGEYIVNTASVAAPDGLGQAAYSASKSGVAGMLPLARELA 180
OY 188 PIGIRVMTIAPGLFGPILTLSPKVCNPLASQVPPPSRLGDPAEYAHVQAIIENPFLN 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 REGIRVMTIAPGLFGPILTLSPKVCNPLASQVPPPSRLGDPAEYAHVQAIIENPFLN 240
OY 248 GEVIRLDGAIIM 259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 GEVIRLDGAIIM 252
```

## RESULT 7

```
O8YBSO PRELIMINARY; PRT; 255 AA.
AC O8YBSO:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100).
GN BME10816.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
OY NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapural V., Redkar R.J., Patra G., Muter C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykdis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DB EMBL: AE009715; AB154058.1; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Oxidoreductase: Complete proteome.
SQ SEQUENCE 255 AA; 26263 MW; 5CF61DAB37F6B730 CRC64;
```

```
Query Match 54.5%; Score 711; DB 16; Length 255;
Best Local Similarity 57.1%; Pred. No. 7.4e-41;
Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

OY 8 VKGLAVITGGASGLATAEIRLVGGASAVLLDLPNSGGEAOKKLGNNVFAADYVS 67
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3 IENKRVLTGSSSGSLGATKALVBOGSKVTLADINAEAGAKAEELGAKRFRAIDIAS 62
OY 68 EKDVOTALAKKGRFGRVAVNCAIGIAVASKTYNLKKGQTHLTEDFORVLDVNLGTFN 127
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 63 DTGKAAIAAIAEAFERIDVLVNCAGVAPAEKV--LGRGAKHLETFRTISINLIGTFN 120
OY 128 VIRLVAGEMGNEPDGQGVYINTASVAFAEGVGQAAYSASKSGITVMTLP1ARDIA 187
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 MRLIAEAMKSNPQGGEGEYIVNTASVAAPDGLGQAAYSASKSGVAGMLPLARELA 180
OY 188 PIGIRVMTIAPGLFGPILTLSPKVCNPLASQVPPPSRLGDPAEYAHVQAIIENPFLN 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 REGIRVMTIAPGLFGPILTLSPKVCNPLASQVPPPSRLGDPAEYAHVQAIIENPFLN 240
OY 248 GEVIRLDGAIIM 259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 GEVIRLDGAIIM 252
```

RESULT 8

O8XWEO PRELIMINARY; PRT; 252 AA.

AC O8XWEO:

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Probable 3-hydroxyacyl-CoA dehydrogenase type II oxidoreductase protein (EC 1.1.1.35).

GN RSC2534 OR RSC05766.

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group; Ralstonia.

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schmitt L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,  
RA Blake J., Bocfield D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibusaki Y., Storch K.-F.,  
RA Suzuki H., Teyo-Oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection";  
RL Nature 409:685-690(2001).  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SBR) FAMILY. BAE28800.1; -  
DR EMBL: AK013340; BAE28800.1; -  
DR HSSP: O70351; IE6W.  
DR MGD: MGI:133871; Hsd17b10.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short; 1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KM Oxidoreductase.  
SQ SEQUENCE 261 AA; 27273 MW; F36CD19C7FEEFAC CRC64;

Query Match 87.7%; Score 1143; DB 11; Length 261;  
Best Local Similarity 87.0%; Pred. No. 3.6e-70;  
Matches 227; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLATAEPLVGGASAVLDPNPGSGGAQAKKGNVVF 60  
DB 1 MAARVSYKGLVAVITGASGLATAEPLVGGASAVLDPNPGSGGAQAKKGESEIF 60  
QY 61 APADVTSEKDVOTATLAKGKFGKRVDAVNCAGIAVASKTYNLKGGTHTEDEFORVLDV 120  
DB 61 APANTSEKELQALTLAKKFGKRDVAVNCAGIAVAKTKHQKKKHTLEDEFORVINY 120  
QY 121 NLMGTFTNIRLVAGMGONPEPDGQGRVYINTASVAEFESQVQAAVSASKGIVGNTL 180  
DB 121 NLTGTFNIRLVAGMGONPEPDGQGRVYINTASVAEFESQVQAAVSASKGIVGNTL 180  
QY 181 PIARDLAFIGIRVMTIAPGLFGLTSLPEKVCNPLASGVPPSRLLDPEVAHLVOAI 240  
DB 181 PIARDLAFIGIRVMTIAPGLFGLTSLPEKVCNPLASGVPPSRLLDPEVAHLVOAI 240  
QY 241 IENPPLNGEVRILDGAIKMP 261  
DB 241 IENPPLNGEVRILDGAIKMP 261

RESULT 4  
Q8TCV9 PRELIMINARY; PRT; 196 AA.  
Q8TCV9;  
AC 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Endoplasmic reticulum-associated amyloid beta peptide-binding protein  
DE (Fragment).  
GN ERAB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Delinger M.H., Meyermann R., Schluessener H.J.;  
RT "Expression, release and induction of endoplasmic reticulum-associated  
RT amyloid beta-binding protein in brain disease";  
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases

DR EMBL: AY092415; AAM18189.1; -  
FT NONTER 196  
SQ SEQUENCE 196 AA; 20581 MW; 2400DE14966BA6A CRC64;

Query Match 75.4%; Score 983; DB 4; Length 196;  
Best Local Similarity 99.5%; Pred. No. 1.8e-59;  
Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 AKRLGNVYFAPADVTSEKDVOTATLAKGKFGKRVDAVNCAGIAVASKTYNLKGGTHT 110  
DB 1 AKRLGNVYFAPADVTSEKDVOTATLAKGKFGKRVDAVNCAGIAVASKTYNLKGGTHT 60  
QY 111 LEDFORVLDVNLMTGTFNIRLVAGMGONPEPDGQGRVYINTASVAEFESQVQAAVSA 170  
DB 61 LEDFORVLDVNLMTGTFNIRLVAGMGONPEPDGQGRVYINTASVAEFESQVQAAVSA 120  
QY 171 SKGGIVGNTLPIARDLAFIGIRVMTIAPGLFGLTSLPEKVCNPLASGVPPSRLLD 230  
DB 121 SKGGIVGNTLPIARDLAFIGIRVMTIAPGLFGLTSLPEKVCNPLASGVPPSRLLD 180  
QY 231 AEYAHVQALLENPFL 246  
DB 181 AEYAHVQALLENPFL 196

RESULT 5  
Q19102 PRELIMINARY; PRT; 258 AA.  
ID Q19102;  
AC 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Probable 3-hydroxyacyl-CoA dehydrogenase f01d4.2 type II (EC 1.1.1.35)  
DE (Type II HADH).  
GN F01G4.2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Harris B.;  
RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA +  
CC NADH.  
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC FAMILY (SDR).  
DR EMBL: Z68341; CA92764.1; -  
DR HSSP: O70351; IE6W.  
DR MGD: MGI:1014.2; CE03127.  
DR WormPep: F01G4.2; CE03127.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short; 1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KM Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.  
FT NP\_BIND 11 36  
FT ACT\_SITE 165 165 NAD (BY SIMILARITY).  
SQ SEQUENCE 258 AA; 27143 MW; 86BF5568EE5902B3 CRC64;

Query Match 57.4%; Score 748; DB 5; Length 258;  
Best Local Similarity 59.9%; Pred. No. 2.3e-43;  
Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;

QY 3 AACRSYKGLVAVITGASGLATAEPLVGGASAVLDPNPGSGGAQAKKLNNVFAP 62  
DB 2 SALRSTGVALVITGASGLATAEPLVGGASAVLDPNPGSGGAQAKKEIG--ITFP 59  
QY 63 ADVTSEKDVOTATLAKGKFGKRVDAVNCAGIAVASKTYNLKGGTHTEDEFORVLDVNL 122  
DB 60 ASVTSEKDVOTATLAKGKFGKRDVAVNCAGIAVAKTKHQKKKHTLEDEFORVINY 119

90 286.5 22.0 254 16 092PP8 rhizobium m  
91 286 21.9 275 16 09K4H0 09K4H0 streptomyc  
92 285.5 21.9 254 16 09RT26 09RT26 delnoccoc  
93 285 21.9 255 16 09PCQ2 09PCQ2 xyella fas  
94 284.5 21.8 257 16 09WYD3 09WYD3 thermotoga  
95 284 21.8 240 16 09AAT3 09AAT3 caulobacter  
96 283.5 21.7 256 17 08TTL5 08TTL5 methanosarc  
97 283 21.7 252 16 092DP0 092DP0 rhizobium m  
98 282.5 21.7 253 16 09CH41 09CH41 lactococcus  
99 282.5 21.7 272 16 099RG1 099RG1 staphylococ  
100 282.5 21.7 521 16 09A7A9 09A7A9 caulobacter

## ALIGNMENTS

## RESULT 1

ID 096HDS PRELIMINARY; PRT; 252 AA.  
AC 096HDS;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Similar to hydroxyacyl-coenzyme A dehydrogenase, type II.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RA Strusberg R.;  
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
(SDR) FAMILY.  
CC EMBL: BC008708; AA08708.1; -;  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short.1.  
DR PROSITE: PS00061; ADH\_SHORT; UNKNOWN\_1.  
KW Oxidoreductase.  
SQ SEQUENCE 252 AA: 25984 MW; F36B71070CE872D CRC64;

Query Match 95.1%; Score 1240.5; DB 4; Length 252;  
Best Local Similarity 96.2%; Pred. No. 8.3e-77;  
Matches 251; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 MAAACRSYKGLVAVITGGASGLGATATRLVGGASAVLLDLPNSGGEAAQAKLGNVVF 60  
DB 1 MAAACRSYKGLVAVITGGASGLGATATRLVGGASAVLLDLPNSGGEAAQAKLGNVVF 60  
QY 61 APADVTSEKDVOTATLAKKFGFRVDVAVNCAGIYVASKTYNLKKGCTHTLEDFORVLDV 120  
DB 61 APADVTSEKDVOTATLAKKFGFRVDVAVNCAGIYVASKTYNLKKGCTHTLEDFORVLDV 120  
QY 121 NMGTFENVIRLVAGEMGONEPDGOGRGVITNTASVAAPFEGVGAASASKSGIYGMTL 180  
DB 121 NMGTFENVIRLVAGEMGONEPDGOGRGVITNTASVAAPFEGVGAASASKSGIYGMTL 180  
QY 181 PIARDLAPITIRVMTTAPGLFTPLTSLPEKVCNFLASQVFPSPRLDPAEYAHLVQAI 240  
DB 181 PIARDLAPITIRVMTTAPGLFTPLTSLPEKVCNFLASQVFPSPRLDPAEYAHLVQAI 240  
QY 241 TENPFLNGEYIRLDGAIKMP 261  
DB 241 TENPFLNGEYIRLDGAIKMP 261

RESULT 2  
Q99N15 PRELIMINARY; PRT; 261 AA.  
AC 099N15;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Short chain L-3-hydroxyacyl-CoA dehydrogenase.  
GN HSD17B10 OR SCHAD.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21098701; PubMed=11165016;  
RA He X.Y., Metz G., Chu C.H., Lin D., Yang Y.Z., Mehta P., Schulz H.,  
RA Yang S.Y.,  
RT Molecular cloning, modeling, and localization of rat type 10 17beta-  
RT hydroxysteroid dehydrogenase.";  
RL Mol. Cell. Endocrinol. 171:89-98(2001).  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
(SDR) FAMILY.  
CC EMBL: AF233685; AAK15008.1; -;  
DR HSSP: C70351; 1E6W.  
DR MGD: MGI:133871; Hsd17b10.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short.1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 261 AA: 27273 MW; F371ED8A15FCEFAF CRC64;

Query Match 88.0%; Score 1147; DB 11; Length 261;  
Best Local Similarity 87.4%; Pred. No. 1.9e-70;  
Matches 228; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 1 MAAACRSYKGLVAVITGGASGLGATATRLVGGASAVLLDLPNSGGEAAQAKLGNVVF 60  
DB 1 MAAACRSYKGLVAVITGGASGLGATATRLVGGASAVLLDLPNSGGEAAQAKLGNVVF 60  
QY 61 APADVTSEKDVOTATLAKKFGFRVDVAVNCAGIYVASKTYNLKKGCTHTLEDFORVLDV 120  
DB 61 APADVTSEKDVOTATLAKKFGFRVDVAVNCAGIYVASKTYNLKKGCTHTLEDFORVLDV 120  
QY 121 NMGTFENVIRLVAGEMGONEPDGOGRGVITNTASVAAPFEGVGAASASKSGIYGMTL 180  
DB 121 NMGTFENVIRLVAGEMGONEPDGOGRGVITNTASVAAPFEGVGAASASKSGIYGMTL 180  
QY 181 PIARDLAPITIRVMTTAPGLFTPLTSLPEKVCNFLASQVFPSPRLDPAEYAHLVQAI 240  
DB 181 PIARDLAPITIRVMTTAPGLFTPLTSLPEKVCNFLASQVFPSPRLDPAEYAHLVQAI 240  
QY 241 TENPFLNGEYIRLDGAIKMP 261  
DB 241 TENPFLNGEYIRLDGAIKMP 261

## RESULT 3

Q9CYT3 PRELIMINARY; PRT; 261 AA.  
AC 09CYT3;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Hydroxyacyl-coenzyme A dehydrogenase, type II.  
GN HSD17B10 OR HADH2.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Thu Jun 26 06:55:11 2003

us-09-931-186-6.rspt

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:22:37 ; Search time 31.6667 Seconds

(without alignments)  
1698.262 Million cell updates/sec

Title: US-09-931-186-6

Perfect score: 1304  
Sequence: 1 MAACRSVKGLVAVTGGAS.....ENPFLNGEVIKLDGAIKMDP 261

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1240.5	95.1	252	4 Q96HDS	Q96HDS homo sapien
2	1147	88.0	261	11 Q99N15	Q99N15 mus musculu
3	1143	87.7	261	11 Q9CVR3	Q9CVR3 mus musculu
4	983	75.4	196	4 Q8RCV9	Q8RCV9 homo sapien
5	748	57.4	258	5 Q19102	Q19102 caenorhabdi
6	720	55.2	255	16 Q910F0	Q910F0 pseudomonas
7	711	54.5	255	16 Q8YBS0	Q8YBS0 bruceella me
8	689.5	52.9	252	16 Q8XW50	Q8XW50 talstonia s
9	675	51.8	255	16 Q92Y51	Q92Y51 rhizobium m
10	671.5	51.5	250	16 Q06544	Q06544 mycobacteri
11	670	51.4	253	16 Q98HM4	Q98HM4 rhizobium l
12	652	50.0	255	2 Q9AHY1	Q9AHY1 pseudomonas
13	642	49.2	257	16 Q8URF2	Q8URF2 agrobacteri
14	607	46.5	126	11 Q9DCX5	Q9DCX5 mus musculu
15	604.5	46.4	264	5 Q8T2T7	Q8T2T7 dictyosteli
16	595	45.6	260	16 Q9AB06	Q9AB06 caulobacter

17	386	29.6	443	2 Q935J3	Q935J3 myxococcus
18	378.5	29.0	246	16 Q8XLD1	Q8XLD1 clostridium
19	360.5	27.6	246	16 Q99YD6	Q99YD6 streptococ
20	355	27.2	252	16 Q9HML5	Q9HML5 pseudomonas
21	343.5	26.3	249	16 Q97DA6	Q97DA6 clostridium
22	340.5	26.1	297	3 Q42774	Q42774 neurospora
23	337.5	25.9	247	16 Q89W0	Q89W0 thermocaneer
24	335	25.7	246	16 Q8K536	Q8K536 bacillus ha
25	334.5	25.7	251	16 Q8YV70	Q8YV70 anabena sp
26	333.5	25.6	246	16 Q9KA03	Q9KA03 bacillus ha
27	331.5	25.4	248	2 Q9KFF1	Q9KFF1 thauera aro
28	330.5	25.3	243	16 Q9PBC3	Q9PBC3 streptococ
29	324.5	24.9	243	16 Q9CHP7	Q9CHP7 lactococcus
30	324.5	24.9	220	16 Q8R068	Q8R068 streptococ
31	324.5	24.8	261	13 Q8U0M4	Q8U0M4 oryzias lat
32	323.5	24.8	260	4 Q96KK9	Q96KK9 homo sapien
33	322	24.7	211	10 Q94G09	Q94G09 cucumis sat
34	321	24.6	263	16 Q9KXW4	Q9KXW4 streptococ
35	320	24.5	262	2 Q9L9F8	Q9L9F8 streptococ
36	319	24.5	271	10 Q94G10	Q94G10 cucumis sat
37	318.5	24.4	251	6 Q8WNN4	Q8WNN4 macaca mul
38	317.5	24.3	246	2 Q9EX74	Q9EX74 rhodococcus
39	317.5	24.3	313	2 Q93HC0	Q93HC0 streptococ
40	316.5	24.3	259	16 Q80616	Q80616 agrobacteri
41	316.5	24.3	296	16 Q9ABX6	Q9ABX6 caulobacter
42	316	24.2	299	17 Q97UK6	Q97UK6 sulfolobus
43	315	24.2	258	2 Q9FRV0	Q9FRV0 streptococ
44	313.5	24.0	260	17 Q8U3B3	Q8U3B3 pyrococcus
45	313	24.0	247	16 Q9PPI6	Q9PPI6 xyella fas
46	312.5	24.0	240	17 Q9U5Y4	Q9U5Y4 pyrococcus
47	312	23.9	237	4 Q8WTW8	Q8WTW8 homo sapien
48	311.5	23.8	249	2 Q9AJT2	Q9AJT2 thauera aro
49	311	23.8	262	16 Q8YD94	Q8YD94 bruceella me
50	310	23.8	253	16 Q8U759	Q8U759 agrobacteri
51	310	23.8	257	10 P93697	P93697 vigna ungui
52	309.5	23.7	244	16 Q8EFT5	Q8EFT5 yersinia pe
53	308.5	23.7	247	16 Q8T690	Q8T690 listeria mo
54	306.5	23.5	247	16 Q92AK1	Q92AK1 listeria in
55	306	23.5	256	16 Q8ZB06	Q8ZB06 yersinia pe
56	305	23.4	250	2 Q56840	Q56840 xanthobacte
57	303.5	23.3	236	11 Q91VT4	Q91VT4 mus musculu
58	303	23.2	248	16 Q8U9B5	Q8U9B5 agrobacteri
59	302.5	23.2	249	2 Q8LBS5	Q8LBS5 geobacillus
60	302	23.2	263	2 Q9S5E7	Q9S5E7 streptococ
61	301	23.1	247	2 Q9ZFP3	Q9ZFP3 bacillus me
62	300.5	23.0	296	5 Q9XX28	Q9XX28 caenorhabdi
63	300	23.0	245	16 Q8YDW1	Q8YDW1 bruceella me
64	300	23.0	252	17 Q97UA4	Q97UA4 sulfolobus
65	298	22.9	273	2 Q9P5T1	Q9P5T1 leifsonia a
66	297.5	22.8	267	2 Q9L3G2	Q9L3G2 streptococ
67	296.5	22.7	258	2 Q8VW75	Q8VW75 mycobacteri
68	295	22.6	260	16 Q9FBT1	Q9FBT1 streptococ
69	294	22.5	255	17 Q9HQ41	Q9HQ41 halobacteri
70	294	22.5	265	16 Q9S2E4	Q9S2E4 streptococ
71	293	22.5	243	16 Q8R625	Q8R625 fusobacteri
72	293	22.5	303	10 Q9SCU0	Q9SCU0 arabidopsis
73	292.5	22.4	255	16 Q8PDG3	Q8PDG3 thermocaneer
74	291	22.3	315	10 Q949M3	Q949M3 brassica na
75	291	22.3	320	10 Q93X62	Q93X62 brassica na
76	290.5	22.3	270	4 Q9UKU3	Q9UKU3 homo sapien
77	290.5	22.3	270	4 Q9BFX1	Q9BFX1 homo sapien
78	290.5	22.3	258	16 Q930L5	Q930L5 rhizobium m
79	290	22.2	272	16 Q8YHE0	Q8YHE0 bruceella me
80	290	22.2	328	10 Q93X67	Q93X67 brassica na
81	290	22.2	246	2 Q9F519	Q9F519 streptococ
82	289.5	22.2	405	16 Q98AS0	Q98AS0 rhizobium l
83	289.5	22.2	246	2 Q93HB3	Q93HB3 streptococ
84	289	22.2	247	2 Q93OF0	Q93OF0 azotobacter
85	288.5	22.1	245	16 Q8R0D9	Q8R0D9 thermocaneer
86	287.5	22.0	246	2 Q9RB80	Q9RB80 burkholderi
87	287.5	22.0	244	16 Q8X815	Q8X815 escherichia
88	286.5	22.0	254	10 Q949M2	Q949M2 brassica na
89	286.5	22.0			

XX 17-JUL-1995; 95WO-GB01678.  
PF  
XX  
PR 20-JUL-1994; 94GB-0014622.  
XX  
PA (ZENEC) ZENEC LTD.  
XX  
PI Chase D, Elborough K, Fentem PA, Slabas AR, White A;  
XX  
DR WPI: 1996-105914/11.  
DR N-PSDB; AAQ93304.  
XX  
PT New isolated rape beta-ketoreductase DNA - used to develop plants  
XX with lower or higher oil contents or with altered oil compsn.  
XX  
PS Claim 1; Page 15; 29pp; English.  
XX  
CC The sequence corresponds to a rape seed beta-ketoreductase encoded  
CC by a cDNA insert in plasmid pRS10.1 in Escherichia coli X11-Blue.  
CC A plastid stroma targeting transit peptide is present. DNA  
CC encoding the protein may be inserted in a vector or expression  
CC cassette in sense or antisense orientation for expression in an  
CC oilseed plant, e.g. for production of transgenic rape plants with  
CC low or modified oil content, diversion of metabolism to alternative  
CC storage compounds, e.g. starch, protein or engineered polymers, or  
CC production of plants with enhanced oil content. The DNA may also  
CC be used as a probe to obtain similar genes from other plants. The  
CC transit peptide may be used to direct other proteins to seed  
CC plastids.  
XX  
SQ Sequence 315 AA:

Query Match 22.7%; Score 296; DB 17; Length 315;  
Best Local Similarity 30.9%; Pred. No. 5.8e-20;  
Matches 81; Conservative 44; Mismatches 115; Indels 22; Gaps 6;  
OY 4 AVRSVKGLVAVITGASGLGLATATRLVGGASAVLLDLPNSGGEA-----QAKKLGNMC 58  
Db 66 AVKVESPPVYVVGASGIGKATATLSL-GKAGCKVLVNTARSAAKEAEVSKQLEAYGGQA 124  
OY 59 VEPADVTSKEDYOTLALAKGKFGRYDVAVNCAITAVASKTYNKKGOTHTLEDFQRYL 118  
Db 125 IIFGGDVSKEDADYEMAKKTATIDAMGTIDVYVNNAGITRDLLIRMKSQ-----WDEVI 178  
OY 119 DVNLMTGFNVIRLVAGEMGNEPDGOGRCVITNTASVAFAEGOVGOAAVSASGSIYGM 178  
Db 179 DLNLITGVFLCTOATKIMMK-----RKRIITINIASVGLIGNICGANTAAKAGVIGF 232  
OY 179 TLPIARDLAPIGIRVMTIAPGLFTPLLSLPKVCNFIASOVPPPSRLGDPAEYAHVQ 238  
Db 233 SKTAARAGSARNTINNVNVCPCGFIASDXTAKIGDMKKIIGTIPL-GRYGQPEDVAGLVE 291  
OY 239 AIIENP---FLNGEVIRLDGAI 257  
Db 292 FLAISPAASYITGCAFTIDGCI 313

Search completed: June 23, 2003, 14:28:28  
Job time : 41.6667 secs



XX 18-DEC-2001 (first entry)

XX Novel human secretory protein, Seq ID No 653.

XX Human: secreted protein; arthritis; Crohn's disease; sepsis; shock;  
KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
KW fertility; analgesic; pain; antigen.

XX Homo sapiens.

XX WO20016689-A2.

XX 13-SEP-2001.

XX 05-MAR-2001, 2001WO-US04942.

XX 07-MAR-2000, 2000US-0519705.

XX 19-MAY-2000, 2000US-0574454.

XX 17-JUN-2000, 2000US-0596193.

XX 14-JUL-2000, 2000US-0616847.

XX 19-SEP-2000, 2000US-0665363.

XX 20-OCT-2000, 2000US-0693267.

XX (HYSEQ) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P,  
PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;  
XX N-PSDB; AAS45196.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries  
PT prepared from various human tissues, for diagnosis and treatment of  
PT cancer, neurological, inflammatory, and autoimmune disorders -

XX Example 2; SEQ ID No 653; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)

XX and polynucleotides (II). (I) and (II) are useful for treating (I)

XX inflammatory conditions such as arthritis, nephritis, Crohn's disease,

XX ischaemia-reperfusion injury, shock, sepsis, immune responses, and is

XX involved in increasing haematopoiesis, stem cell survival, bone growth

XX and remodeling. (I), (II) and modulators of (II) are useful for

XX prophylaxis or treatment of one or more cancers. (II) is also useful for

XX creating transgenic animals useful for studying the in vivo activities of

XX the polypeptide as well as for studying modulators of the polypeptides.

XX (I) induces the proliferation of neural cells and regeneration of nerve

XX and brain tissue and is useful for the treatment of central and

XX peripheral nervous system diseases and neuropathies, such as Alzheimer's,

XX Parkinson's disease, Huntington's disease, and amyotrophic lateral

XX sclerosis. In addition, (I) is involved in chemotactic or chemokinetic

XX activity, regulation of haematopoiesis and is useful for treating myeloid

XX or lymphoid cell disorders, platelet disorders such as thrombocytopenia

XX and for regeneration of bone, cartilage, tendon, ligament and/or nerve

XX tissue growth, and in tissue repair, healing of burns, incisions,

XX ulcers, for treating osteoporosis, osteoarthritis, bone degenerative

XX disorders, or periodontal disease. Furthermore, (I) is also useful for

XX gut protection or regeneration and treatment of lung or liver fibrosis,

XX reperfusion injury in various tissues, various immune deficiencies and

XX disorders including severe combined immunodeficiency (SCID), bacterial or

XX fungal infections, autoimmune disorders e.g. multiple sclerosis,

XX rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic

XX reactions and conditions, such as asthma or other respiratory problems.

XX In addition, (I) affects biorythms or circadian cycles of rhythms,

XX fertility, metabolism, catabolism, anabolism, storage or elimination of

XX dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides

CC analgesic effects or other pain reducing effects, immunoglobulin like  
CC activity and can act as an antigen in a vaccine composition to raise an  
CC immune response. AAU28020-AAU28395 represent novel human secreted protein  
CC amino acid sequences of the invention.

XX Sequence 288 AA:

Query Match 23.1%; Score 301.5; DB 22; Length 288;

Best Local Similarity 29.9%; Pred. No. 1.5e-20;

Matches 84; Conservative 44; Mismatches 110; Indels 43; Gaps 6;

1 MAAAVRSYKGLVAVITGASGLGATATRLVGGASAVLDPNSGGEPAKRLGNCF 60

10 MATGTR-YAGKAVAVTGGGRIAGIYRAFVNSGARVYCDKDESGRALEQELPGCL 68

61 APADYTSKDVOTATLAKGKRGVDAVNVNAGIAVASKITNKKGQHTLEDFORVLDV 120

69 SCDVTOEDDVKTLVSETIRRFGRUDCVNNAHHPP-ORPETSAGFRQDEL 123

121 NLMTGFNYIRLVAGMGONEPDGORGVIINTASVAAFEGOVQOAAVSASKGIVGTL 180

124 NLGTYTLTKLALPYLRKSQ-----GNVINISLVGALGOAAVPAVATKGAVTAMTK 176

181 PIARDLPIGIRVMTIARGLFTPLTSLPEKVCNPLASQVFP----- 224

177 ALALDESPGVKRVNCSIGNITWPLMEF-----LALMPDPATTRBSMLAQRSGV 228

225 -----SRGDPAEY-AHLVCAITENPFLNGEYIRLDGAIM 259

229 QIQPLGRMGOPAEVGAAGAAVFLASEANFCTGIXLTVTGAE 269

RESULT 23

ID AA95746 standard; Protein; 247 AA.

AA95746;

25-OCT-2000 (first entry)

Bacillus megaterium 3-keto-acyl-CoA reductase Phab.

Polyhydroxyalkanoate: polyhydroxybutyrate; transgenic plant; Phab;

Bacillus megaterium.

WO200040730-A1.

13-JUL-2000.

07-JAN-2000; 2000WO-US00364.

07-JAN-1999; 99US-0115592.

(UYMA-) UNTV MASSACHUSETTS.

Cannon MC, Cannon FC, Mccool GJ, Valentin HE, Gruys KJ;

WPI: 2000-532624/48.

N-PSDB; AAS50142.

New nucleic acid fragment encoding proteins involved in

polyhydroxyalkanoate (PHA) biosynthesis, useful in the production of

transgenic plants or recombinant plant cells which can express PHAs

such as polyhydroxybutyrate -

Claim 85; Page 137-138; 153pp; English.

The present sequence is that of Phab, a 3-keto-acyl-CoA-reductase

protein of Bacillus megaterium. The sequence was deduced from an

open reading frame identified in an isolated 7,916 bp fragment of

B. megaterium strain 11561 genomic DNA (see AAS50142). The 7,916 bp

```

PR 05-APR-1999; 990P-0098205.
XX
XX (DAIL ) DAICEL CHEM IND LTD.
XX
XX Yamamoto H;
XX
XX WPI: 2000-118183/11.
XX N-PSDB; AA245749.
XX
XX Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -
XX
XX Claim 6; Page 19-20; 34pp; English.
XX
XX The present sequence represents a beta-ketoacyl-ACP reductase protein
XX of Bacillus subtilis. The beta-ketoacyl-ACP reductase enzyme constitutes
XX a Type II fatty acid synthetase. The enzyme has an extremely high
XX reducing activity and stereoselectivity towards 4-chloroacetoacetic
XX acid ester. The specification describes a method for producing a
XX (S)-4-halo-3-hydroxybutyric acid ester. The method comprises
XX asymmetrically reducing 4-halo-acetoacetic acid ester or its
XX derivative with beta-ketoacyl-acyl carrier protein reductase
XX constituting Type II fatty acid synthase, or acetoacetyl-CoA
XX reductase constituting the polybeta-hydroxy fatty acid biosynthesis
XX system. The novel method is used to produce optically active
XX 4-halo-3-hydroxybutyric acid ester, with a high purity.
XX
SQ Sequence 248 AA;

Query Match 23.8%; Score 310.5; DB 21; Length 248;
Best Local Similarity 29.7%; Pred. No. 1.7e-21;
Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;

QY 13 AVITGGASGLAETAEERLVGQASAVLIDLPSNGGEAOA-----KKIGNNCVAPADY 65
DB 9 AITWGSRSIGSIALALAKSGANV---VNSGNEAKNEVDEIKSGRAIAVKADY 65
QY 66 TSEKDVOTALAKGKFGKRVAVNAGIYAVASKTYNKKGGTHLLEPQRLDYNLNGI 125
DB 66 SNEDVQNNIKETLSFTIIDLNNAGITRNLIMRKE-----DEMDVYINLNGV 119
QY 126 FNVIRLVAGEGQNEPDGQGRGVIIINTASVAEFGVQQAASASKGIVGMLPIARD 185
DB 120 FNCTKAVTRQMKQ-----RSGRILNVSIIIVGSGNPGQANYVAAKAGVIGLTRKSAKE 173
QY 186 LAPIGIRVMTIAPGLGFTPLSLPEKVCNFLASQVPPSRIGDPAEVAHIVQAIIEN-- 243
DB 174 LMSRNTTVAAIAPGFIISTDMTDLAKDYDEMLKQIPL-ARGGEPSDVSSVYTFLASGA 232
QY 244 PFLNGEVIRLDGAIRM 259
DB 233 RYMTGOTLHDGGMV 248

RESULT 21
ABBA48892
ID ABBA48892 standard; Protein; 247 AA.
AC ABBA48892;
XX
XX 05-FEB-2002 (first entry)
XX
XX Listeria monocytogenes protein #1596.
XX
XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
XX vitamin B12; bacterial infection; disease.
XX
XX Listeria monocytogenes.
XX
XX WO200177335-A2.
XX
XX 18-OCT-2001.
XX
XX 11-APR-2001; 2001WO-FR01118

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XX
XX 11-APR-2000; 2000FR-0004629.
XX
XX (INSP ) INST PASTEUR.
XX
XX Buchrieser C, Frangoul L, Couve E, Rusniok C, Faïh H, Deboux P,
XX Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P,
XX Daniels J, Goebel W, Kieft J, Kuhn M, Ng E, Vazquez-Boland JA,
XX Dominguez-Bernal G, Garrido-Garcia P, Tleieriz-Martinez A, Amend A,
XX Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L,
XX Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N,
XX Madueno E, De Pablos B, Wehland J, Kaerst U, Ertlan K, Hauf J,
XX Rose M, Voss H;
XX
XX WPI: 2002-010914/01.
XX
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX and prevention of Listeria and related bacterial infections, and
XX related polypeptides -
XX
XX Claim 6; SEQ ID No 1597; 192pp; French.
XX
XX The present invention relates to the genome sequence of Listeria
XX monocytogenes EGD-e (see AB03041). The genome sequence and fragments of
XX it are useful for selecting probes and primers for detecting genes in L.
XX monocytogenes and related organisms, and for studying genetic
XX polymorphisms and other genomes. The present sequence is a protein
XX encoded by the genome sequence of the present invention. Proteins
XX expressed from the genome sequence are useful for raising specific
XX antibodies, identification of L. monocytogenes and related organisms, and
XX for biosynthesis and biodegradation, especially biosynthesis of Vitamin
XX B12. The genome sequence and proteins encoded by it are also useful for
XX selecting compounds that regulate gene expression and cell replication
XX and modulate L. monocytogenes-related diseases. In addition, the genome
XX sequence and proteins encoded by it are useful in pharmaceutical and
XX vaccines compositions for the treatment or prevention of infections by L.
XX monocytogenes and related organisms.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 247 AA;

Query Match 23.3%; Score 303.5; DB 23; Length 247;
Best Local Similarity 32.0%; Pred. No. 8.1e-21;
Matches 85; Conservative 45; Mismatches 103; Indels 33; Gaps 7;

QY 7 SVKGLVAVTGGASGLAETAEERLVGQASAVLIDLPSNGGEAOA-----KKL-----GNNC 58
DB 2 TLQGVAVVMTGSGRIGRIDAINLAKEGANIFF---NYGSPAAEETAKIAAEHGEV 57
QY 59 VFAPADYSEKDVOTALAKGKFGKRVAVNAGIYAVASKTYNKKGGTHLLEPQRLD 118
DB 58 EAKRANVAIADVDVAFRQALIERGRVYDILVNNAGITRNLIMRKE-----DEMDVY 111
QY 119 DVNLGFTNVIRLVAGEGQNEPDGQGRGVIIINTASVAEFGVQQAASASKGIVG 178
DB 112 NINLKGFTLCRAVSRFMKQ-----RAGKIIMASVVGILGNAGQANYVASRAGVIGL 165
QY 179 TLPIARDIAPIGIYVMTIAPGLGFTPLSLPEKVCNFLASQVPPSRIGDPAEVA 238
DB 166 TKTTAREIAPRGINVAVAPGFIITDMTDLKDKETKRAMAQIP-----LGAYGTEDIAN 221
QY 239 AII-----ENPFLNGEVIRLDGAIRM 259
DB 222 AVLFLASDASKYITGOTLSVDGGMV 247

RESULT 22
AAU28296
ID AAU28296 standard; Protein; 288 AA.
AC AAU28296;
XX

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QY 187 APGIRVMTAPGLFGTPLLTSLPEKVCNFIASQVPPSPRIGDPAEVAHIVQATIIENPFL 246  
 DB 167 ARKKIRVAVAPGVVHDMTKLEE--HLKKNIPL-GRGETIEVAHAHVFLLESPIYI 222  
 QY 247 NGEVIRLDGAIIR 259  
 DB 223 TGHVLVVDGGLQL 235  
 RESULT 19  
 ID AAU28344 standard; Protein: 257 AA.  
 XX  
 AC AAU28344;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Novel human secretory protein, Seq ID No 701.  
 XX  
 KW Human: secreted protein; arthritis; Crohn's disease; sepsis; shock;  
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
 KW fertility; analgesic; pain; antigen.  
 XX  
 OS Homo sapiens.  
 PN WO200166689-A2.  
 PD 13-SEP-2001.  
 PF 05-MAR-2001; 2001MO-US04942.  
 XX  
 PR 07-MAR-2000; 2000US-0519705.  
 PR 19-MAY-2000; 2000US-0574454.  
 PR 17-JUN-2000; 2000US-0596193.  
 PR 14-JUL-2000; 2000US-0616847.  
 PR 19-SEP-2000; 2000US-0665363.  
 PR 20-OCT-2000; 2000US-0693267.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P,  
 PI Zhao QA, Yang Y, Dimañac RT, Zhang J, Chen R, Xue AJ, Wang J;  
 XX  
 DR N-PDB: AAS45244.  
 DR WPI: 2001-589934/66.  
 XX  
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries  
 PT prepared from various human tissues, for diagnosis and treatment of  
 PT cancer, neurological, inflammatory, and autoimmune disorders -  
 XX  
 PS Example 2; SEQ ID No 701; 107pp; English.  
 XX  
 CC The invention relates to novel isolated human secreted polypeptides (I)  
 CC and polynucleotides (II). (I) and (II) are useful for treating  
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,  
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is  
 CC involved in increasing haematopoiesis, stem cell survival, bone growth  
 CC and remodeling. (I), (II) and modulators of (II) are useful for  
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for  
 CC creating transgenic animals useful for studying the in vivo activities of  
 CC the polypeptide as well as for studying modulators of the polypeptides.  
 CC (I) induces the proliferation of neural cells and regeneration of nerve  
 CC and brain tissue and is useful for the treatment of central and  
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,  
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral  
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis and is useful for treating myeloid

CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
 CC tissue growth, and in tissue repair, healing of burns, incisions,  
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative  
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for  
 CC gut protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues, various immune deficiencies and  
 CC disorders including severe combined immunodeficiency (SCID), bacterial or  
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,  
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic  
 CC reactions and conditions, such as asthma or other respiratory problems.  
 CC In addition, (I) affects biophysics or circadian cycles of rhythms,  
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of  
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides  
 CC analgesic effects or other pain reducing effects, immunoglobulin like  
 CC activity and can act as an antigen in a vaccine composition to raise an  
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein  
 CC amino acid sequences of the invention.  
 XX  
 SQ Sequence 257 AA;  
 Query Match 23.9%; Score 312; DB 22; Length 257;  
 Best Local Similarity 31.6%; Pred. No. 1.3e-21;  
 Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;  
 QY 12 VAVITGASGLGATAEELVGGASAVLLDLPNSGGEAOKKIGNNCFAPADVTSEKDV 71  
 DB 24 VCAVFGSGSRGIGRAVAOIMARKGRIYAIRNLEGAKAAGDGGDHLAFSCVAKSHDV 83  
 QY 72 OTALAKKGRFGRVAVNAGI-----AVASKYNNLKKQOTHTLEDFQVLDVNLMTGF 126  
 DB 84 ONTEFEMKHLGRNPLVNAAGIRBDLYRKT-----EDMQQLHNLIGSM 122  
 QY 127 NVIRLVAGENGQNPDDGGGGRVITNTASVAAEQGVQGAAYASAKGIGMTLPARDL 186  
 DB 133 LTCKAARTMTQ-----OGGSIVNNGSIYGLKNGSGQSVYASAKGLVGFSLAKREV 186  
 QY 187 APGIRVMTAPGLFGTPLLTSLPEKVCNFIASQVPPSPRIGDPAEVAHIVQATIIENPFL 246  
 DB 187 ARKKIRVAVAPGVVHDMTKLEE--HLKKNIPL-GRGETIEVAHAHVFLLESPIYI 242  
 QY 247 NGEVIRLDGAIIR 259  
 DB 243 TGHVLVVDGGLQL 255  
 RESULT 20  
 ID AAU28344 standard; Protein: 248 AA.  
 XX  
 AC AAU28344;  
 XX  
 DT 06-APR-2000 (first entry)  
 XX  
 DE Amino acid sequence of a beta-ketoacyl-ACP reductase protein.  
 XX  
 KW Beta-ketoacyl-ACP reductase: Type II fatty acid synthetase;  
 KW stereospecificity; 4-chloroacetoacetic acid ester;  
 KW (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;  
 KW beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase;  
 KW polybeta-hydroxy fatty acid biosynthesis; optically active;  
 KW 4-hol-3-hydroxybutyric acid ester.  
 XX  
 OS Bacillus subtilis.  
 PN EP955375-A2.  
 PD 10-NOV-1999.  
 PF 10-MAY-1999; 99EP-0109403.  
 PR 08-MAY-1998; 98JP-0126507.  
 PR 21-OCT-1998; 98JP-0300178.



Best Local Similarity 32.0%; Pred. No. 7.6e-22;  
Matches 81; Conservative 41; Mismatches 105; Indels 26; Gaps 5;

```
QY 12 VAVITGGAGSGGLAERLVGOGASAVLLDLPNSGGEAOAKLGNVCYFADPTSEKDV 71
D 4 VCAITGGSGIGRAVAQIMARKGRALIAIRLDEAKAKAAGLDGDLAFSCDVAKEHDV 63
QY 72 QALALAKKGFGRVDVAVNCAGI-----AVASKTYNLKKGCTHTLEDFORVLDTLMGTF 126
D 64 QNTPEMEKHGIRVNFVNAAGINDSLVPRKT-----EDWVSQLHTNLLGSM 112
QY 127 NVIRLVAGMGONEPDGGGQGVITNTASVAAFESQVQGAAYASAKSGIVGMLTPIARDL 186
D 113 LKCKAMRAMIQ-----QGGSIVNVGSIVGLKNGNSQSVYASAKSGLVGFSRALAKEV 166
QY 187 ADIGIRVNTIAPGLFPTPLTSLPEKVCNFTASQVPPSRIGDPFAVHAHVQATIENTEPL 246
D 167 AKKIRVNVVAPGPFVHTDKLKEE---HLKKNIPL-GRGGETLEVAAHVFLLESPTI 222
QY 247 NGEVIRLDGAIRM 259
D 223 TGHVLVVDGGLQL 235
```

## RESULT 16

AAB96397  
ID AAB96397 standard; Protein; 241 AA.

AC AAB96397;  
DT 29-OCT-2001 (first entry)

DE Putative P. abyssi dehydrogenase #8.

KM Hyperthermophilic archaeon; hyperthermophilic protein.

OS Pyrococcus abyssi.

PN FR2792651-A1.

PD 27-OCT-2000.

PF 21-APR-1999; 99FR-0005034.

PR 21-APR-1999; 99FR-0005034.

PA (CNRS) CNRS CENT NAT RECH SCI.

PI (IFRE-) IFREMER INST FR RECH EXPL MER.

PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;  
Quereillon J, Weissenbach J, Saurin W, Hellig R;

DR WPI; 2001-126236/14.

PT New nucleotide sequences isolated from Pyrococcus abyssi encode  
proteins useful in industry -

PS Claim 7; Pages 1087-1088; 1657pp; French.

CC The present invention relates to the genomic sequence of Pyrococcus

CC abyssi (see AAB96431 and AAB4123-7) and P. abyssi proteins. P. abyssi is

CC a hyperthermophilic archaeon, which is isolated from deep-sea

CC hydrothermal vents. The present sequence is one such P. abyssi protein.

CC The proteins of the present invention have various potential industrial

CC uses, since the proteins are stable at very high temperatures, some up to

CC 110 degrees centigrade.

CC Note: This patent is in the same patent family as WO2000055062, which

CC contains additional sequences as shown in AAB99132-AAB99143,

CC AAH75903-AAH75920 and AAG66436.

XX Sequence 241 AA;

Query Match 24.0%; Score 313.5; DB 22; Length 241;

Best Local Similarity 35.3%; Pred. No. 8.7e-22;  
Matches 91; Conservative 44; Mismatches 88; Indels 35; Gaps 8;

```
QY 8 VKGLVAVITGGAGSGGLATIERLVGOGASAVLLDLPNSGGEAOAKLGNVC-----VF 60
D 4 LKGVAVITGGASRGIGRAIAIEIAKRGVNVVIRNSN---EEBAKTEELCRQYGVETLL 60
QY 61 APADVTEKDVQATLAKKGFGRVDVAVNCAGIATVNAKKTGCTHTLEDFORVLDT 120
D 61 VKADVSNREVRKRVKVIDKFRIDILLNAGI--LGKI---KDLPLVDEMDRYISV 115
QY 121 NMGTFNVIRLVAGMGONEPDGGGQGVITNTASVAAFESQVQGAAYASAKSGIVGMLT 180
D 116 NLKGAFTVQGEVLRYM-----KKKKTIVNIASIKGKGGVGPFYASAKSGLLALTF 166
QY 181 PIARDLPIGIRVNTIAPGLFPTPLTSLPEKVCNFTASQVPPSRIGD---PAVHAHV 237
D 167 NLAHPLAP-NLVNAVAPGPVDIDMLSEKMKIKKL-----SLGDIAPKPSVAAHV 218
QY 238 QATIENTEPLNGEVIRLDG 255
D 219 IFLLENDHITGEVIDVANG 236
```

## RESULT 17

AAU28156  
ID AAU28156 standard; Protein; 237 AA.

AC AAU28156;

DT 18-DEC-2001 (first entry)

DE Novel human secretory protein, Seq ID No 325.

KM Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;

KM ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;

KM transgenic animal; Alzheimer's disease; Parkinson's disease; burn;

KM amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease;

KM gut protection; lung; liver fibrosis; immune deficiency; infection;

KM severe combined immunodeficiency; SCID; autoimmune disorder; allergy;

KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;

KM fertility; analgesic; pain; antigen.

XX Homo sapiens.

OS Homo sapiens.

PN WO200166689-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US04942.

PR 07-MAR-2000; 2000US-0519705.

PR 19-MAY-2000; 2000US-0574454.

PR 17-JUN-2000; 2000US-0596193.

PR 14-JUL-2000; 2000US-0616847.

PR 19-SEP-2000; 2000US-0665363.

PR 20-OCT-2000; 2000US-0693267.

XX (HTSE-) HTSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

XX Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX N-PSDB; AAS45056.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries

XX prepared from various human tissues, for diagnosis and treatment of

XX cancer, neurological, inflammatory, and autoimmune disorders -

XX Example 4; SEQ ID No 325; 107pp; English.

```

XX      Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI      Yamamoto RT, Xu HH;
XX      WPI: 2001-611495/70.
DR      N-PSDB: AAS53187.
XX      New polynucleotides for the identification and development of
PT      antibiotics, comprise sequences of antisense nucleic acids -
PS      Example 3; Seq ID No 10921; 511bp; English.
XX      The invention relates to antisense inhibitors of genes essential to
CC      prokaryotic cellular proliferation, their use in identifying the
CC      genes, their use in the discovery of novel antibiotics, the essential
CC      genes themselves and the encoded proteins. The prokaryotes used are
CC      Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC      pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC      invention is also useful for the identification of potential new targets
CC      for antibiotic development. The antisense nucleic acids can also be used
CC      to identify proteins used in proliferation, to express these proteins,
CC      and to obtain antibodies capable of binding to the expressed proteins.
CC      The proteins can be used to screen compounds in rational drug discovery
CC      programmes. The antisense nucleic acid sequence is also useful to screen
CC      for homologous nucleic acids which are required for cell proliferation in
CC      a wide variety of organisms. The present sequence represents an
CC      essential prokaryotic cellular proliferation protein.
CC      Note: The sequence data for this patent did not form part
CC      of the printed specification, but was obtained in electronic
CC      format directly from WIPO at:
CC      ftp.wipo.int/pub/published_pct_sequences.
XX      Sequence 245 AA:
SQ
Query Match      24.4%; Score 318.5; DB 22; Length 245;
Best Local Similarity 33.7%; Pred. No. 3e-22;
Matches 84; Conservative 38; Mismatches 108; Indels 19; Gaps 5;
QY      15 ITGGASGGLTAERLVGGASAVLID---LPNSGGEPQAKKLGNCVAPADYTSKRD 70
DB      10 ITGSGTGIKAAVALFAKKEGANIVLNGRSEITPEOROEIEA--FEVCKIGISGDDSDDA 67
QY      71 VQATALAKRGKRDVAIVACAGIVASRTYVLKKGRTHTEPDRVADVNLNGFENVIR 130
DB      68 AGEMIAITVDQLGSDILDVNNAGIT-----NDKLLIKTKEDFNACDINLVGTFNNMQ 121
QY      131 LVAGENGQNEPDGQGRVYINTASVAAEFGVGQAAYSASKGIVGKMTLPARDLADIG 190
DB      122 QAVKRMKMO-----RSGRITIMNASVSGIMGVQANVAASKAGVYGFTKSVAREVAPRG 175
QY      191 IRYMTAPLFGPPLITFSPEKVCNPLASQVPEPRILGDPAPAYALHVAIITNPLNGEV 250
DB      176 ITCNATAPFPIQTMTDVLSEKVKQANQIPLQT-FGQVEVAATATFLAKSPITTCOV 234
QY      251 IRDGAIRM 259
DB      235 VAVDGLVM 243
RESULT 15
AAMS0255
ID      AAMS0255 standard; Protein; 237 AA.
XX      AAMS0255;
AC      AAMS0255;
DT      21-JAN-2002 (first entry)
XX      Human dehydrogenase 21509.
XX      Dehydrogenase; human; ovarian cancer; colon cancer; lung cancer;
KW      liver cancer; metastasis; antitumor; therapy; diagnosis.
XX      OS      Homo sapiens.

```

```

XX      Key
FH      Domain
FT      Location/Qualifiers
FT      3..229
FT      /note="short-chain alcohol dehydrogenase domain"
FT      148..158
FT      /note="short-chain alcohol dehydrogenase family
FT      signature"
FT      Modified-site
FT      114..116
FT      /note="O-phosphorylated by protein kinase C"
FT      Modified-site
FT      66..69
FT      /note="O-phosphorylated by casein kinase II"
FT      Modified-site
FT      95..98
FT      /note="O-phosphorylated by casein kinase II"
FT      Modified-site
FT      9..14
FT      /note="N-myristoylated"
FT      Modified-site
FT      38..43
FT      /note="N-myristoylated"
FT      Modified-site
FT      110..115
FT      /note="N-myristoylated"
FT      Modified-site
FT      128..133
FT      /note="N-myristoylated"
FT      Modified-site
FT      134..139
FT      /note="N-myristoylated"
FT      Modified-site
FT      153..158
FT      /note="N-myristoylated"
XX      MO200175119-A2.
XX      11-OCT-2001.
XX      02-APR-2001; 2001WO-US10720.
XX      31-MAR-2000; 2000US-193920P.
XX      (MILL-) MILLENNIUM PHARM INC.
XX      Meyers RA, Rudolph-Owen LA;
XX      WPI: 2001-626438/72.
XX      N-PSDB: AAI70573.
XX      Novel isolated 21509 and 33770 polypeptides belonging to human
PT      dehydrogenase family members, useful for treating cancer, diabetes,
PT      atherosclerosis, glomerulonephritis, Crohn's disease, cirrhosis,
PT      multiple sclerosis -
XX      Claim 1(a): Fig 2; 146pp; English.
XX      The present sequence is that of a novel human dehydrogenase,
CC      designated 21509. The protein has a significant number of
CC      structural characteristics in common with members of the
CC      dehydrogenase/oxidoreductase family. Its expression pattern
CC      suggests a role in tumour development. The invention provides
CC      21509 and 33770 nucleic acids, antisense molecules, recombinant
CC      expression vectors, host cells and transgenic animals in which a
CC      21509 or 3370 gene has been introduced or disrupted. It also
CC      provides 21509 and 33770 proteins, fusion proteins, antigenic
CC      peptides and antibodies, and methods for screening for compounds
CC      that modulate the expression or activity of 21509 or 33770
CC      polypeptides or nucleic acids. Such modulators are used in methods
CC      for inhibiting the proliferation or migration, or inducing the
CC      killing, of 21509- or 33770-expressing cells, especially the
CC      hyperproliferative and/or metastatic cells of a soft tissue tumour,
CC      solid tumour or metastatic lesion, especially ovarian cancer, colon
CC      cancer, lung cancer and liver cancer (claimed). Modulator
CC      compounds are also used in claimed methods of modulating fatty acid
CC      biosynthesis or retinoid biosynthesis in a cell. 21509 and 33770
CC      nucleic acids can also be used to prepare diagnostic probes and in
CC      gene (including antisense) therapy.
XX      Sequence 237 AA;
SQ
Query Match      24.1%; Score 314; DB 22; Length 237;

```





XX Streptococcus pneumoniae.  
OS  
XX  
XX WO200044885-A1.  
XX  
XX 03-AUG-2000.  
XX  
XX 19-JAN-2000; 2000WO-US01131.  
XX  
XX 27-JAN-1999; 99US-0239052.  
XX  
XX (SMK ) SMITHKLINE BEECHAM CORP.  
XX  
XX Holmes DJ, Mooney J, Zhong YF, Debouck C, Jaworski D, Wang M,  
PI Warren RL, Kosmicka AL, McDevitt D, Ingraham KA, Chalker AF;  
PI So CY, Wallis NG, Pearson SC;  
XX  
XX MPI: 2000-482971/42.  
XX  
XX N-PSDB: AAA74684.  
XX  
XX FabG polypeptide, isolated from Streptococcus pneumoniae, is used to  
PT treat microbial diseases, identify agonists and antagonists for  
PT treating microbial infections and to detect diseases associated with  
PT microbial infections -  
XX  
XX  
XX Claim 1; Page 3; 40pp; English.  
XX  
XX The present sequence is a FabG (2-oxoacyl-acyl carrier protein  
CC reductase) polypeptide. A full length FabG gene was isolated from a  
CC Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG  
CC polynucleotides and polypeptides are used for detection and treatment of  
CC microbial diseases. They may also be used to identify antagonists and  
CC agonists which can then be used to treat microbial diseases. Compounds  
CC that interfere with the initial physical interaction between a pathogen  
CC and a host have been identified. The compounds are able to prevent the  
CC adhesion of bacteria to mammalian extracellular proteins in wounds,  
CC prevent adhesion between mammalian extracellular proteins and bacterial  
CC FabG proteins which mediate tissue damage and/or to block normal  
CC progression of pathogenesis in infections mediated by implantation of  
CC in-dwelling devices or other surgical techniques. The FabG  
CC polypeptides, polynucleotides, antagonists and agonists are especially  
CC useful in the treatment of Helicobacter pylori infection. They may be  
CC used to decrease H. pylori-induced cancers and to prevent, inhibit  
CC and/or cure gastric ulcers and gastritis.  
XX  
XX Sequence 243 AA;  
SQ  
Query Match 25.0%; Score 326.5; DB 21; Length 243;  
Best Local Similarity 35.1%; Pred. No. 5e-23;  
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

AAU37767  
ID AAU37767 standard; Protein; 243 AA.  
XX  
XX  
XX AAU37767;  
AC  
XX  
XX 14-FEB-2002 (first entry)  
DT  
XX  
XX Streptococcus pneumoniae cellular proliferation protein #196.  
DE  
XX  
XX Antisense: prokaryotic cellular proliferation protein;  
XX antibiotic; antibacterial; drug design.  
XX  
XX Streptococcus pneumoniae.  
OS  
XX  
XX WO200170955-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 21-MAR-2001; 2001WO-US09180.  
XX  
XX 21-MAR-2000; 2000US-191078P.  
XX  
XX 23-MAY-2000; 2000US-206848P.  
XX  
XX 26-MAY-2000; 2000US-207727P.  
XX  
XX 23-OCT-2000; 2000US-242578P.  
XX  
XX 27-NOV-2000; 2000US-253625P.  
XX  
XX 22-DEC-2000; 2000US-257931P.  
XX  
XX 16-FEB-2001; 2001US-269308P.  
XX  
XX (ELITRA) ELITRA PHARM INC.  
XX  
XX Haselbeck R, Ohlsen KU, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;  
XX  
XX MPI: 2001-611495/70.  
XX  
XX N-PSDB: AAS55626.  
XX  
XX New polynucleotides for the identification and development of  
PI antibiotics, comprise sequences of antisense nucleic acids -  
XX  
XX Example 3; Seq ID No 13360; 511pp; English.  
XX  
XX The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the  
CC genes, their use in the discovery of novel antibiotics, the essential  
CC genes themselves and the encoded proteins. The prokaryotes used are  
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella  
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The  
CC invention is also useful for the identification of potential new targets  
CC for antibiotic development. The antisense nucleic acids can also be used  
CC to identify proteins used in proliferation, to express these proteins,  
CC and to obtain antibodies capable of binding to the expressed proteins.  
CC The proteins can be used to screen compounds in rational drug discovery  
CC programmes. The antisense nucleic acid sequence is also useful to screen  
CC for homologous nucleic acids which are required for cell proliferation in  
CC a wide variety of organisms. The present sequence represents an  
CC essential prokaryotic cellular proliferation protein.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 243 AA;  
SQ  
Query Match 25.0%; Score 326.5; DB 22; Length 243;  
Best Local Similarity 35.1%; Pred. No. 5e-23;  
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;



XX New Streptococcus protein for the treatment or prevention of infection  
PT or disease caused by Streptococcus bacteria, such as meningitis, and  
PT for detecting a compound that binds to the protein -  
XX  
XX  
PS Claim 1: Page 3542; 4525pp; English.  
XX  
CC The invention relates to a protein (ABP25413-ABP30895) from group B  
CC Streptococcus/GBS (Streptococcus agalactiae) or group A Streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and anti-inflammatory  
CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and  
CC antibodies that bind (1) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (1) are used to detect Streptococcus in a  
CC biological sample. (1) is used to determine whether a compound binds to  
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (1) may be used to recombinantly produce (1) and may be  
CC used in gene therapy. Antibodies to (1) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins.  
CC  
SQ Sequence 243 AA;  
XX  
XX  
Query Match 26.9%; Score 351; DB 23; Length 243;  
Best Local Similarity 35.4%; Pred. No. 2.3e-25;  
Matches 92; Conservative 42; Mismatches 100; Indels 26; Gaps 6;  
XX  
QY 8 VAGLAVITGGASGLTAERLVGGASAVLLDPNSGGEQAOKL-----GNCVF 60  
DB 3 IKGNI-FITGSTRGIGLMAHQFASLEANIIVL-----NGRSATSEELVASFPTYVT 56  
XX  
QY 61 AAPDVTSERDQATLAKGKFGVDVAVNCAGIAVASKTYLKKGGQTHTEDFORVLDV 120  
DB 57 ISGDVSEABKRMVMEALIESISIDVLYNNAGIT-----NDKLMKTEBDFRYLKI 110  
XX  
QY 121 NIMGTEVIRLVAGENGONEPDGGRGVIINTASVAAFEQGVGAASASRGGIVGML 180  
DB 111 NLTGAENMTQSVL-----KPMIKARQGAIIINSSVVGILGNIGQANVAAASKRAGIGFTK 164  
XX  
QY 181 PIARDLAPIGIRMTAPGLFGPPLTSLPEKVCNFIASQVPPPSLGDPAFYAHLYQAI 240  
DB 165 SVAREVAAARICVNAIAPGFIESDMGVLPKKQEQIISQIPM-KRIGKAQEVAAHLASF 223  
XX  
QY 241 IENPFLNGEYIRLDGAIRM 260  
DB 224 VEDDYITIGVIAIDGSM 243  
XX  
XX  
RESULT 8  
ID AAM80670 standard; Protein: 243 AA.  
XX  
AC AAM80670;  
XX  
XX  
DT 24-DEC-1998 (first entry)  
XX  
DE S. pneumoniae fatty acid biosynthesis protein.  
XX  
KW Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;  
KW virulence; antibody; infection; detection; treatment; hypothetical;  
KW cell wall biosynthetic, external target; minimal gene set protein.  
XX  
OS Streptococcus pneumoniae.  
XX  
PN WO9826072-A1.  
XX  
PD 18-JUN-1998.  
XX  
PF , 09-DEC-1997; 97MO-US22578.

XX  
FR 13-DEC-1996; 96US-0036281.  
XX  
PA (EUIL ) LILLY & CO ELI.  
XX  
PI Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR;  
PI Mills RJ, Norris PH, Peery RB, Rockey PK, Rostock PR;  
PI Skettrud PL, Smith MC, Solenberg PJ, Treadway RJ;  
PI Young Bellido ML.  
XX  
DR WPI; 1998-348529/30.  
XX  
PT Streptococcus pneumoniae nucleic acid sequences - used in DNA chips  
PT for evaluating gene expression, and identification of virulence  
PT genes  
XX  
PS Claim 3; Page 270; 333pp; English.  
XX  
XX  
CC This sequence represents a S. pneumoniae fatty acid biosynthesis  
CC protein. The invention provides DNA sequences (AAV65201 to AAV65304)  
CC from the Streptococcus pneumoniae genome and corresponding protein  
CC sequences (AAM80605 to AAM80728). The protein sequences are classified as  
CC hypothetical, cell wall biosynthetic, external target, or minimal gene  
CC set proteins. A recombinant host containing a vector comprising any of  
CC the above nucleic acids can be used for the recombinant expression of the  
CC proteins. The invention also provides a DNA chip having arrayed on it at  
CC least 15 base pair fragment of any one or more of these DNA sequences.  
CC The DNA chip can be used methods for evaluating gene expression in S.  
CC pneumoniae and for identifying virulence genes in S. pneumoniae.  
CC Antibodies that selectively bind to the above proteins or peptide  
CC fragments can be used to treat S. pneumoniae infection. The antibodies  
CC can also be used to detect S. pneumoniae cells.  
XX  
SQ Sequence 243 AA;  
XX  
XX  
Query Match 25.0%; Score 326.5; DB 19; Length 243;  
Best Local Similarity 35.1%; Pred. No. 5e-23;  
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;  
XX  
QY 15 ITGASGLGLTAERLVGGASAVLLDPNSGGE-----AQAKKLNCCVFPADVTSE 68  
DB 10 ITGSSRGIGLTAERLVGGASAVLLDPNSGGE-----NSRGAISEELVAFESNYIKVPPSGDVSDP 65  
XX  
QY 69 KDVCATLALAKGKFGVDVAVNCAGIAVASKTYLKKGGQTHTEDFORVLDVNLMTGFNV 128  
DB 66 ADARMTDQAIAELGSDVLYNNAGIT--TQDTLMKMA-----TEADFEKVLKVNLTGAFNM 119  
XX  
QY 129 IRLVAGENGONEPDGGRGVIINTASVAAFEQGVGAASASRGGIVGMLPIARDLAP 188  
DB 120 TQSVL-----KPMKARQGAIIINSSVVGILGNIGQANVAAASKRAGIGFTKSVAREVAS 173  
XX  
QY 189 IGIRMTAPGLFGPPLTSLPEKVCNFIASQVPPPSLGDPAFYAHLYQAIINPFLNG 248  
DB 174 ENIRVNTAPGMISDMTALISDXIKERTLAQIPM-KEFGADEVADLIYFLAGQDYL 232  
XX  
QY 249 EVIRLDGAIRM 259  
DB 233 QVIAIDGGLSM 243  
XX  
XX  
RESULT 9  
ID AAB15706 standard; Protein: 243 AA.  
XX  
AC AAB15706;  
XX  
XX  
DT 07-DEC-2000 (first entry)  
XX  
DE Streptococcus pneumoniae Fabg polypeptide.  
XX  
XX  
KW Streptococcus pneumoniae; Fabg; 3-oxoacyl-acyl carrier protein reductase;  
KW antibacterial; cytostatic; anticancer; cancer; gastric ulcer; gastritis;  
KW Helicobacter pylori infection; microbial infection.



	CC	the treatment or prevention of infection or disease caused by
	CC	Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
	CC	Nucleic acids encoding (I) are used to detect Streptococcus in a
	CC	biological sample. (I) is used to determine whether a compound binds to
	CC	(I). A composition comprising (I) or a nucleic acid encoding (I), may be
	CC	used as a vaccine or diagnostic composition. The disease caused by
	CC	Streptococcus that is prevented or treated may be meningitis. Nucleic
	CC	acid encoding (I) may be used to recombinantly produce (I) and may be
	CC	used in gene therapy. Antibodies to (I) are used for affinity
	CC	chromatography, immunoassays, and distinguishing/identifying
	CC	Streptococcus proteins.
XX	Sequence	244 AA:
SQ	Query Match	27.7%; Score 361.5; DB 23; Length 244;
	Best Local Similarity	36.5%; Pred. No. 2.3e-26;
	Matches	92; Conservative 38; Mismatches 99; Indels 23; Gaps 5;
OY	15	ITGASGIGLATARLVGGASAVLLDPNNGE-----AQARKIGNNCVFAPADATSE 68
Dd	10	ITGSSRGIGLAIHQFALGANIVL----KRSISEDLIEPFDYGKVVAISGVSSF 65
OY	69	KDVQTALALAKGFGRVDVAVNCAGIAVASKTYNIKKGQHTLEDFOHVIDYNIMGFNV 128
Dd	66	EDARRMEIKELIASLSGYDVLVNNAGIT-----NDKLMLKMTVEEFESVLKINLGAFNM 119
OY	129	IRLVAGEKGQNEPPQGQGGVLIIMTASYAFAPEGVGQAAYASASKGIYGMFLPTARDLAP 188
Dd	120	TGSVL-----KPMTKAROGAILINSSVGLGTGNVCANVYASRAGLIGFTKSAREVYA 173
OY	189	IGIRVMTIAPGLFGTPILTLSPERVCNFLASQVFPFSRLGDPAEYAHLVQAIIENPLNG 248
Dd	174	RGIIRNALAAPGISMDMVDVIPKMOEAIIAQIDM-KRIKGKKEVAQVASFLEAEQEVLTG 232
OY	249	EVRILDGAIRMQ 260
Dd	233	QVIALDGGMTWQ 244
RESULT 7		
ID	ABP27345	
AC	ABP27345 standard; Protein; 243 AA.	
XX	ABP27345;	
DT	02-JUL-2002 (first entry)	
XX	Streptococcus polypeptide SEQ ID NO 3866.	
DE		
XX	Streptococcus; GAS; GBs; group B streptococcus; Streptococcus agalactiae;	
KN	group A streptococcus; Streptococcus pyogenes; antibacterial;	
KM	antiinflammatory; Infection; vaccine; meningitis; gene therapy.	
XX	Streptococcus pyogenes.	
OS		
PN	WO200234771-A2.	
PD	02-MAY-2002.	
XX	29-OCT-2001; 2001WO-GB04789.	
PE	27-OCT-2000; 2000GB-0026333.	
PR	24-NOV-2000; 2000GB-0028727.	
XX	07-MAR-2001; 2001GB-0005640.	
XX	(CHUR-) CHIRON SPA.	
PA	(GENO-) INST GENOMIC RES.	
XX	Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;	
PI	Tettelin H;	
XX		
DR	WPI: 2002-352536/38.	
	N-PSDB: ABN67976.	

CC (see AAX00611 for described uses).

XX Sequence 227 AA:

Query Match 87.9%; Score 1146; DB 20; Length 227;  
Best Local Similarity 100.0%; Pred. No. 2.5e-101;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ASAVILDLPSNGGEAQAQKRIKNNCPAPADVTSEKVCYRLALAKKRFGRVAVAVACAI 94  
DB 1 ASAVILDLPSNGGEAQAQKRIKNNCPAPADVTSEKVCYRLALAKKRFGRVAVAVACAI 60  
QY 95 AVASKTYNLKKGQTHLEDFQRYLDVNLKMGTFNVIRLVAGEMQNEPDGQGRGYIINTA 154  
DB 61 AVASKTYNLKKGQTHLEDFQRYLDVNLKMGTFNVIRLVAGEMQNEPDGQGRGYIINTA 120  
QY 155 SVAAFEGQVQAAYASAKSGIVGNTLPFIARDLPFGIRVYVTPAGLFGPILTSLEPKYC 214  
DB 121 SVAAFEGQVQAAYASAKSGIVGNTLPFIARDLPFGIRVYVTPAGLFGPILTSLEPKYC 180  
QY 215 NFLASQVFPFSLGDPAPFAVLAHVQALLENPFNGEVRILDGAIKMP 261  
DB 181 NFLASQVFPFSLGDPAPFAVLAHVQALLENPFNGEVRILDGAIKMP 227

RESULT 4  
ABB62988

ID ABB62988 standard; Protein: 255 AA.

XX ABB62988;

XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 15756.

KM Drosophila; developmental biology; cell signalling; insecticide;  
pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-655860/75.

XX N-PSDB; ABL07091.

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
genes from Drosophila and for elucidating cell signalling and cell-cell  
interactions -

PS Disclosure: SEQ ID NO 15756; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA  
sequences (AB101840-AB116175) and the encoded proteins  
(AB157737-AB172072).

CC The sequence data for this patent did not form part of the printed  
specification, but was obtained in electronic format directly from WIPO  
at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 255 AA:

Query Match 69.6%; Score 908; DB 22; Length 255;  
Best Local Similarity 68.9%; Pred. No. 1.6e-78;  
Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VGLFAVITGGASGGLTAERLYQGASAVLLDLPNSGGEAQAQKRIKNNCPAPADVT 67  
DB 2 IKNAVSLVTGGASGIGRAIETRIAKQASVILLADLPSSKGVAKELGDKVFPVAVTS 61  
QY 68 EKDVQALALAKGKFRVAVAVNCAGIYAVASKTYNLKKGQTHLEDFQRYLDVNLKMGTFN 127  
DB 62 EKDVSAALQTAADKFGRLDLPVNCAGIYAVASKTYNLKKGQTHLEDFQRYLDVNLKMGTFN 121  
QY 128 VIRLVAGEMQNEPDGQGRGYIINTASVAFEGQVQAAYASAKSGIVGNTLPFIARDLA 187  
DB 122 VIRLSAGLGMANEPMDGQGRGYIINTASVAFEGQVQAAYASAKSGIVGNTLPFIARDLS 181  
QY 188 PIGIRVMTIAPGLFGPILTSLEPKVCNFLASQVFPFSLGDPAPFAVLAHVQALLENPF 247  
DB 182 TQIRICTIAPGLFMTMPMLALPEKVRTEFLAKSIFPQRLGSEYAHVQALYIENPFLN 241  
QY 248 GEVIRIDGAIKMP 261  
DB 242 GEVIRIDGAIKMP 255

RESULT 5  
AAM06513

ID AAM06513 standard; Protein: 388 AA.

XX AAM06513;

XX 08-MAR-1997 (first entry)

DE Flavobacterium ORF-5 gene product.

KM Carotenoid; lycopene; beta-carotene; echinenone; canthaxanthin;

KW zeaxanthin; adonixanthin; astaxanthin.

OS Flavobacterium sp. R1534 WT (ATCC 21568).

XX EP747483-A2.

XX 11-DEC-1996.

XX 29-MAY-1996; 96EP-0108556.

XX 09-JUN-1995; 95EP-0108888.

XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.

PI Hohmann H, Pasamontes L, Tessier M, Van Loon A;

XX WPI; 1997-023160/03.

XX N-PSDB; AAT45143.

PT Flavobacterium gene sequences encoding carotenoid biosynthesis  
enzymes - for the production of carotenoid(s), useful in foods and  
animal feeds

PS Example 2; Fig 7; 80pp; English.

XX A polypeptide (AAM06513) showing approx. 30% homology to

CC streptomycete polyketide synthases was identified as the product

CC of ORF-5 from a carotenoid gene cluster (see also AAT45143) of

CC Flavobacterium sp. R1534. 5 Other open reading frames of the

CC gene cluster coded for carotenoid biosynthetic enzymes (see also  
AAM06515-18 and AAM00871) and can be used to produce carotenoids in  
transformed host cells.

XX Sequence 388 AA;

FT		/note= "alpha helix region A"	
FT	Region	190..196	
FT		/note= "beta sheet region F"	
FT	Region	204..218	
FT		/note= "alpha helix region F"	
FT	Region	247..252	
FT		/note= "beta sheet region G"	
XX			
PX	M09954347-A2.		
PD	28-OCT-1999		
PF			
PE	19-APR-1999;	99WO-EP02610.	
PR	17-APR-1998;	98US-0082257.	
XX			
PA	(HORM-) INST HORMON & FORTEPFLANZUNGSFORSCHUNG GM.		
PI	Ivell R, Spiess A, Balvers M, Jaehner D, Hansis C;		
XX			
DR	NFI; 2000-052699/04.		
XX	N-PSTDB; AA34663.		
XX			
PT	Novel differential display reverse transcription PCR method used to		
PT	detect genes expressed in mutant tissues		
PS	Claim 4; Fig 2; 40pp; English.		
XX			
CC	This sequence represents murine Alzheimer-associated beta-amyloid		
CC	binding protein (ERAB, see AA32239), a novel member of the SCAD		
CC	(short chain alcohol dehydrogenase) family of steroid metabolizing		
CC	and related enzymes. The sequence was deduced from cDNA (see		
CC	AA234663) identified using a novel differential display RT-PCR method		
CC	for analysis of w/wv mouse testis gene products. ERAB is		
CC	specifically upregulated in the testicular Leydig cells of w/wv		
CC	aospermic mutant mice, suggesting an important role in the		
CC	establishment and support of spermatogenesis. The invention also		
CC	relates to vectors, host cells, methods for expressing the ERAB		
CC	nucleic acid, and antibodies. The nucleic acid and protein are		
CC	useful e.g., as markers for testicular development.		
XX			
SQ	Sequence	260 AA:	
	Query Match	88.1%; Score 1149; DB 21; Length 260;	
	Best Local Similarity	88.0%; Pred. No. 1.5e+101;	
	Matches 227; Conservative 18; Mismatches 13; Indels 0; Gaps 0		
OY	4 AVMSVGGIYAIVITGAGSGIGLATARLYGCAASAVILDLNPGSEGAOKKLGNNCFAPA	63	
Db	3 AVRSVGGLAIVAVTGGASGLGTAKRLVGCGATNVLDVPDSBEAQAKLGSCLIFADA	62	
OY	64 DVASEDVQFATALAKKGKEGRDYVANVCAGIAVASKEYTNLKGGTHTLEDFOVLVDNIM	123	
Db	63 NVTSEREIQDALTLANEKRGEDIVAVNCAGIAVAIKTHCKKNRIHTLEDFQAVINWLI	122	
OY	124 GTFNVRIRLVAGEMGONEPPDGGORVVINTNTSAVFAGGVGOQAAYSSKGGIYGMLPLA	183	
Db	123 GTFNVRIRLVAGEMGONEPPDGGORVVINTNTSAVFAGGVGOQAAYSSKGGIYGMLPLA	182	
OY	184 RDLAPIGIRMYMTIAPGLFGTPLLSLSPKYCNFLASGVPPSRUGDAEYAHVQAIIEN	243	
Db	183 RDLAPIGIRMYMTIAPGLFGTPLLSLTPKYCNFLASGVPPSRUGDAEYAHVQAIIEN	242	
OY	244 PFLNGEVIRLDGAIKMP 261		
Db	243 PFLNGEVIRLDGAIKMP 260		
XX			
RESULT 3			
ID	AA067934		
XX	AA067934 standard; Protein; 227 AA.		
XX			

XX	25-MAR-1999	(first entry)	
DI	Fragment of human secreted protein encoded by gene 8.		
XX	Human, secreted protein; fusion protein; gene therapy; protein therapy;		
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia		
KW	developmental abnormality; fetal deficiency; blood; allergy; renal;		
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;		
KW	inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;		
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus		
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;		
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.		
XX	Homo sapiens.		
OS	WO9842738-A1.		
PN	01-OCT-1998.		
XX	19-MAR-1998;	98WO-US05311.	
PF	30-MAY-1997;	97US-0050937.	
XX	PR 21-MAR-1997;	97US-0041276.	
XX	PR 21-MAR-1997;	97US-0041277.	
XX	PR 21-MAR-1997;	97US-0041281.	
XX	PR 21-MAR-1997;	97US-0042344.	
XX	PR 30-MAY-1997;	97US-0048069.	
XX	PR 30-MAY-1997;	97US-0048094.	
XX	PR 30-MAY-1997;	97US-0048095.	
XX	PR 30-MAY-1997;	97US-0048096.	
XX	PR 30-MAY-1997;	97US-0048131.	
XX	PR 30-MAY-1997;	97US-0048135.	
XX	PR 30-MAY-1997;	97US-0048154.	
XX	PR 30-MAY-1997;	97US-0048160.	
XX	PR 30-MAY-1997;	97US-0048186.	
XX	PR 30-MAY-1997;	97US-0048187.	
XX	PR 30-MAY-1997;	97US-0048188.	
XX	PR 30-MAY-1997;	97US-0048350.	
XX	PR 30-MAY-1997;	97US-0048351.	
XX	PR 30-MAY-1997;	97US-0048352.	
XX	PR 30-MAY-1997;	97US-0048355.	
XX	PR 05-AUG-1997;	97US-0054804.	
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX	Brewer LA, Duan R, Ehner R, Ferrie AM, Florence KA;		
XX	Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;		
PI	Rosen CA, Ruben SM, Shi Y, Young P;		
XX	WPI; 1999-070066/06.		
DR	N-PDB; AAX00618.		
XX	New isolated human genes and the secreted polypeptides they encode -		
PT	useful for diagnosis and treatment of e.g. cancers, neurological		
PT	disorders, immune diseases, inflammation or blood disorders		
PS	Disclosure; Page 11; 385pp; English.		
XX	This sequence represents a fragment of a secreted human protein encoded		
CC	by the nucleic acid molecule detailed in the descriptor line. The gene		
CC	can be used to generate fusion proteins by linking to the gene to a		
CC	human immunoglobulin Fc portion (e.g. AAX00602) for increasing the		
CC	stability of the fused protein as compared to their fragments (nucleic		
CC	acid sequences: AAX00611-X00724; amino acid sequences AAM67807-W68004)		
CC	which are useful for preventing, treating or ameliorating medical		
CC	conditions e.g. by protein or gene therapy. Also, pathological		
CC	conditions can be diagnosed by determining the amount of the new		
CC	polypeptides in a sample or by determining the presence of mutations in		
CC	the new polynucleotides. Specific uses are described for each of the 87		
CC	polynucleotides based on which tissues they are most highly expressed		

84	265.5	20.4	246	22	AAE02195	S. aureus NADPH-de
85	265.5	20.4	268	22	ABE52552	Escherichia coli p
86	264	20.2	247	16	AAE66291	Mycobacterium bovi
87	264	20.2	247	16	AAE63899	M. Bovis p55 ORF1
88	264	20.2	247	18	AAE40809	M. Bovis p55 opeto
89	264	20.2	276	21	AAE54416	Secoisolaricidresin
90	264	20.2	276	23	AAO21494	Secoisolaricidresin
91	263	20.2	261	13	AAE27556	NAD affinity glucoc
92	262.5	20.1	252	23	AAO16940	Recombinant enzyme
93	261	20.0	272	21	AAE10740	B. megaterium gluc
94	261	20.0	277	21	AAE54413	Secoisolaricidresin
95	261	20.0	340	21	AAE10741	H. gillii/anti/B. me
96	260.5	20.0	273	21	AAE54414	Secoisolaricidresin
97	260	19.9	243	23	ABE54107	Lactococcus lactis
98	259	19.9	253	22	AAU36249	Pseudomonas aerugi
99	258	19.8	283	21	AAE31552	Arabidopsis thalia
100	258	19.8	283	23	ABE92823	Herbicideally activ

## ALIGNMENTS

## RESULT 1

AAW71471 standard; Protein; 261 AA.

AAW71471;  
16-DEC-1998 (first entry)  
ERAB protein.

Endoplasmic reticulum associated amyloid-beta peptide binding protein;  
ERAB protein; amyloid-beta peptide inhibitor; demyelinating disease;  
neurodegenerative disorder; therapy; Alzheimer's disease; schizophrenia;  
Down's syndrome; Parkinson's disease; Huntington's disease;  
multiple sclerosis.

Homo sapiens.

MO9840484-A1.

17-SEP-1998.

12-MAR-1998; 98WO-US04915.

12-MAR-1997; 97US-0815225.

(UYCO ) UNIV COLUMBIA NEW YORK.

Stern DM, Yan SD;

WPI: 1998-531524/45.

N-PSSB; AAV60576.

Endoplasmic reticulum associated amyloid-beta peptide binding

protein - inhibitors of which can be used to treat neurodegenerative

disorders

Claim 2; Fig 1D; 53pp; English.

This sequence is the endoplasmic reticulum associated amyloid-beta  
peptide binding (ERAB) protein of the invention. The protein can be used  
in a method for evaluating the ability of an agent to inhibit binding of  
ERAB polypeptide to amyloid-beta peptide comprising: (a) incubating the  
ERAB polypeptide, the agent and amyloid-beta peptide under binding  
conditions; (b) determining the amount of amyloid-beta peptide bound to  
ERAB polypeptide; (c) comparison of the amount of binding with results  
from a control using no agent, so determining inhibition ability of the  
agent. The inhibitors identified by the method can be used to treat a  
neurodegenerative condition by administration of an agent that inhibits  
binding of an ERAB polypeptide to amyloid-beta peptide, particularly,

disease, Huntington's disease, schizophrenia, a demyelinating disease, or  
multiple sclerosis. The inhibitors can also be used to treat other  
neurodegenerative conditions including those associated with ageing,  
dentatorubral and pallidolysian atrophy, Machado-Joseph disease,  
muscular dystrophy, senility, spinocerebellar ataxia type I, spinobulbar  
muscular atrophy, stroke, and trauma.

SQ Sequence 261 AA;

Query Match 99.6%; Score 1299; DB 19; Length 261;  
Best Local Similarity 99.6%; Pred. No. 7 3e-116;  
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MAAAVSVKGLVAVITGASGLGLATAEERLVGGASAVLLDLPNSGGEAAKKGNNVF	60
Db	1	MAAACSVKGLVAVITGASGLGLATAEERLVGGASAVLLDLPNSGGEAAKKGNNVF	60
QY	61	APADVTSEKDVOTLALAKKFGFVDVAVNACAGIAVASKTYNKKQTHLEDFORVLDV	120
Db	61	APADVTSEKDVOTLALAKKFGFVDVAVNACAGIAVASKTYNKKQTHLEDFORVLDV	120
QY	121	NLMGTENVIRLVAGENGQNEPDGOGGVIIINTASVAEFGVGQAAYSASKGIVGML	180
Db	121	NLMGTENVIRLVAGENGQNEPDGOGGVIIINTASVAEFGVGQAAYSASKGIVGML	180
QY	181	PIARDLAPIGIRMTAPGIFGTPLTSLPEKCNFLASGVPPSRFGPAEYAHVQAI	240
Db	181	PIARDLAPIGIRMTAPGIFGTPLTSLPEKCNFLASGVPPSRFGPAEYAHVQAI	240
QY	241	IENPFLNGEVIRLDGAIKMP	261
Db	241	IENPFLNGEVIRLDGAIKMP	261

## RESULT 2

AAV32239 standard; Protein; 260 AA.

AAV32239;

15-FEB-2000 (first entry)

Alzheimer-associated beta-amyloid binding protein (ERAB).

Alzheimer-associated beta-amyloid binding protein; ERAB; mouse;

Leydig cell; differential display RT-PCR; DDRT-PCR;

short chain alcohol dehydrogenase; SCAD; testis; marker;

spermatogenesis.

Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

FT	Region	Location/Qualifiers
FT	Region	10..15
FT	Region	/note= "beta sheet region A"
FT	Region	18..32
FT	Region	/note= "alpha helix region A"
FT	Region	35..41
FT	Region	/note= "beta sheet region B"
FT	Region	43..57
FT	Region	/note= "alpha helix region B"
FT	Region	61..66
FT	Region	/note= "beta sheet region C"
FT	Region	70..80
FT	Region	/note= "alpha helix region C"
FT	Region	84..94
FT	Region	/note= "beta sheet region D"
FT	Region	109..133
FT	Region	/note= "alpha helix region D"
FT	Region	143..153
FT	Region	/note= "beta sheet region E"
FT	Region	157..171
FT	Region	/note= "SCAD motif"

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:21 ; Search time 39.6667 Seconds  
(without alignments)  
876.767 Million cell updates/sec

Title: US-09-931-186-4  
Perfect score: 1304  
Sequence: 1 MAANVRVKGLAVITGAS.....ENPLNGEVIRLDIAIMQP 261

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

A:Geneseq.101002:\*

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13: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1972.DAT:\*  
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23: /SID22/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1299	99.6	261	19	AAW71471
2	1149	88.1	260	11	AAV32239
3	1146	87.9	227	20	AAW67934
4	908	69.6	255	22	ABB62988
5	664.5	51.0	388	18	AAW06513
6	361.5	27.7	244	23	ABP28011
7	351	26.9	243	23	ABP27345
8	326.5	25.0	243	19	AAW80670
9	326.5	25.0	243	21	AAW15706
10	326.5	25.0	243	22	AAU37767

11	326.5	25.0	243	22	AAU37988
12	325.5	25.0	243	22	AAW01032
13	324.5	24.9	243	23	ABW54087
14	318.5	24.4	245	22	AAU53328
15	314	24.1	237	22	AAW50255
16	313.5	24.0	241	22	AAW63977
17	312	23.9	237	22	AAU28156
18	312	23.9	237	22	AAU19928
19	312	23.9	257	22	AAU28344
20	310.5	23.8	248	21	AAV54422
21	303.5	23.3	247	23	ABW48892
22	301.5	23.1	288	22	AAU82966
23	301	23.1	247	21	AAV95746
24	296	22.7	315	17	AAW9323
25	296	22.7	315	17	AAW9322
26	295	22.6	263	23	ABP9667
27	294	22.5	262	22	AAW63032
28	293.5	22.5	267	22	AAW47459
29	292.5	22.4	262	22	AAW6337
30	291.5	22.4	270	20	AAV41761
31	291.5	22.4	270	21	AAW44317
32	291.5	22.4	270	21	AAW44056
33	291.5	22.4	270	21	AAW28108
34	291.5	22.4	279	22	AAU18296
35	289.5	22.2	244	21	AAV54421
36	289.5	22.2	244	21	AAU34533
37	288.5	22.1	246	12	AAU10974
38	288.5	22.1	262	21	AAV44578
39	288	22.1	263	10	AAU38499
40	287.5	22.0	246	10	AAW4157
41	287.5	22.0	246	14	AAW2192
42	287.5	22.0	246	20	AAV3310
43	287.5	22.0	246	21	AAV54423
44	287.5	22.0	246	22	AAW1981
45	287.5	22.0	270	21	AAW42558
46	287.5	22.0	277	21	AAV54415
47	287.5	22.0	303	13	AAW2654
48	287.5	22.0	329	16	AAW1324
49	285.5	21.7	253	23	ABW54214
50	282.5	21.7	273	10	AAW94155
51	282	21.6	280	23	ABW92449
52	280.5	21.5	254	22	AAW49773
53	280.5	21.5	306	22	AAW81644
54	279.5	21.4	241	12	AAU10679
55	278.5	21.4	242	22	AAU59290
56	278.5	21.4	244	23	ABP9586
57	278	21.3	244	22	AAW81318
58	276	21.2	258	22	AAW92682
59	276	21.2	258	22	AAW9361
60	276	21.2	285	22	AAU34668
61	275	21.1	246	14	AAW74761
62	274.5	21.1	254	22	AAW47522
63	274.5	21.1	269	23	ABW52448
64	274	21.0	206	23	AAU99345
65	273.5	21.0	249	23	ABP9980
66	273.5	21.0	272	22	AAU37095
67	273	20.9	202	23	AAU77210
68	272.5	20.9	286	22	AAU6267
69	271.5	20.8	251	22	AAU41193
70	270.5	20.7	267	21	AAW35505
71	270.5	20.7	308	21	AAW35504
72	269.5	20.7	246	21	AAW15707
73	269.5	20.7	246	22	AAU33965
74	269.5	20.7	246	22	AAU36530
75	269.5	20.7	246	22	AAU37210
76	269.5	20.7	246	22	AAU37507
77	269.5	20.6	231	22	ABP9552
78	268.5	20.6	248	20	AAV6959
79	268	20.6	186	19	AAW38474
80	267.5	20.5	166	21	AAW32509
81	267.5	20.5	336	16	AAW06488
82	266.5	20.4	242	22	AAU53381
83	266	20.4	254	23	ABW48207

Streptococcus pneu  
CFE 35 proteic seq  
Lactococcus lactis  
Enterococcus faeca  
Human dehydrogenas  
putative P. abyssal  
Novel human secret  
Human oxireducta  
Novel human secret  
Amo acid sequenc  
Listeria monocytog  
Novel human secret  
Bacillus megaterium  
Rape leaf beta-ket  
Staphylococcus epi  
S. epidermidis ope  
Levodione reductas  
G. suboxydans DSM  
Human PRO474 (UNO5  
Human PRO474 prote  
Novel human secret  
Human endocrine po  
Amino acid sequenc  
E. coli cellular p  
Acetoacetyl COA re  
Xylitol dehydrogen  
Salmonella typhi c  
Acetyl COA reducta  
Sequence encoded b  
Acetoacetyl COA re  
Amino acid sequenc  
Ralstonia eutropha  
Human ORFX CRP2322  
Secoliparicidresin  
Hericidially activ  
Acetyl COA reducta  
Lactococcus lactis  
Acetyl COA reducta  
Hericidially activ  
Protein with acetyl  
S. epidermidis ope  
Acetoacetyl COA re  
Propionibacterium  
Staphylococcus epi  
Human AFP protein  
C glutamicum prote  
Corynebacterium g1  
E. coli cellular p  
Acetoacetyl COA re  
(R)-2-octanol dehy  
Hericidially activ  
Short-chain dehydr  
Staphylococcus epi  
Staphylococcus aut  
Staphylococcus aut  
Staphylococcus aut  
Staphylococcus epi  
Staphylococcus epi  
Chlamydia trachoma  
S. pneumoniae 3-ox  
Human OXRE-6. Hom  
Maize T82 sequence  
Haemophilus influe  
Listeria monocytog

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Search completed: June 23, 2003, 14:35:39  
Job time : 13.1667 secs

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Page 11

REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50475  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 270:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 186 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6348328e  
US-08-856-270

Query Match 20.6%; Score 268; DB 4; Length 186;  
Best Local Similarity 38.7%; Pred. No. 7.7e-22;  
Matches 74; Conservative 23; Mismatches 72; Indels 22; Gaps 5;

QY 15 ITGASGGLATAEERLVGOGASAVLLDLPNSGGE-----AQAKLGNVCYFAPADVTSE 68  
DB 10 ITGSSRGIGLAIHKEFAQGANIVL-----NSRGAISEELLAEFSNYGKRVVPISGDSDF 65  
QY 69 KVVQALALAKKFRGVAVVACGIAVASKTYNLKKGQHTLEDFQVLDVNLMTGTVN 128  
DB 66 AAKKRIIDQAIHLEGSVDVLYNNAGI---TQDTLMKMK---TEADFEKVLKYNLTGAFNM 119  
QY 129 IRLVAGEMQNEPDGQGGGVIIINTASVAFAFEGVQGAAYSASKGIYGMPLPIARDIAP 188  
DB 120 TQSVL-----KPKMKAREGAIINMSVYGLMGNIGQANYASAKGLIGFTKSVAREVAS 173  
QY 189 IGRVMTIAPG 199  
DB 174 RNIIRVNIAPG 184

RESULT 24

US-08-440-856A-3  
Sequence 3, Application US/08440856A  
Patent No. 5750873  
GENERAL INFORMATION:  
APPLICANT: DELAPORTA, STEPHEN L.  
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING  
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 2000 PENNSYLVANIA AVE. N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,856A  
FILING DATE: 15-MAY-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A.  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 05463-20001.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1517  
TELEFAX: (202) 887-0763  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-440-856A-3

Query Match 20.5%; Score 267.5; DB 1; Length 337;  
Best Local Similarity 30.9%; Pred. No. 2.2e-21;  
Matches 88; Conservative 44; Mismatches 112; Indels 41; Gaps 6;

QY 6 RSVKGLVAVITGASGGLATAEERLVGOGASAVLLDLPNSGGEQAQKLGNNVCYFAPADY 65  
DB 51 KRLDGKVAIYTGARGIGEAIVLEFAKHGARVYIADIDDAAGBALSAALGPQVSEFRCV 110  
QY 66 TSEKDVQFALALAKGR-GRVDYAVNACGIAVASKTYNLLKKGQHTLEDFQVLDVNLMTG 124  
DB 111 SVEDDVRAVDVMSLRGRLDYCNNAV-LGRQTPAARSITLSDAEEDRVLRYNALG 169  
QY 125 TFNVIIRLVAGEMQNEPDGQGGGVIIINTASVAFAFEGVQGAAYSASKGIYGMPLPIAR 184  
DB 170 AALGKHAARAPR-----RAGSIYSVASVAIVGLGPHAYTASKAHVAIGLTKNPAAC 223  
QY 185 DLAPIGIRVMTIAPGLFTPL-----TSLF-----EX 212  
DB 224 ELRAHGVAVNCVSFEVATPMLINARQGHDDATADRDLDLDLVTPSDQVEKME 283  
QY 213 VCNFLASQVFPFPRSLGPAEYAHVQAIIENPFLNGEVIRLDGAI 257  
DB 284 VVRGLATLKGPTLRPRDIAE-AVLFLASDEARYISGHNLVYDGV 327

RESULT 25

US-09-504-358-14  
Sequence 14, Application US/09504358  
Patent No. 6365376  
GENERAL INFORMATION:  
APPLICANT: Rouviere, Pierre E.  
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIA  
FILE REFERENCE: BCI001 US NA  
CURRENT FILING DATE: 2000-02-15  
EARLIER APPLICATION NUMBER: US/09/504,358  
CURRENT FILING DATE: 2000-02-15  
EARLIER FILING DATE: 1999-February-19  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 14  
LENGTH: 256  
TYPE: PRT  
ORGANISM: Brevibacterium sp HCU  
US-09-504-358-14

Query Match 20.4%; Score 266; DB 4; Length 256;  
Best Local Similarity 30.9%; Pred. No. 2.1e-21;  
Matches 82; Conservative 39; Mismatches 116; Indels 28; Gaps 8;

QY 10 GLVAVITGASGGLATAEERLVGOGASAVLLDLPNSGGEQAQKLGNNVCYFAPADY 66  
DB 6 KRVAVITGASGGMGRIQSELASBGAQVAVDVADQEGRAADAIASGGAANYWKLDVS 65  
QY 67 SEKDVQFALALAKGRFGRVDYAVNACGIAVASKTYNLLKKGQHTLE--DFQVLDVNLMTG 124  
DB 66 DESEVEIIVSDIAKFRGAINVLYNNAGVTGDK-----PTHEIDERDLDLVISDVKG 118  
QY 125 TFNVIIRLVAGEMQNEPDGQGGGVIIINTASVAFAFEGVQGAAYSASKGIYGMPLPIAR 184  
DB 119 VFTMKRHCIPYKQ---AGG--GAIIVFAISIIYGVSGDELTPHAAAGAVALLTKDAY 172  
QY 185 DLAPIGIRVMTIAPGLFTPLTSLPEK-----VCNFLASQVFPFPRSLDPAEY--AH 235  
DB 173 TYGPNIRVNNVAPGTITPLVKELSGRPGDLGTYKIMGAKHPL-GRVGTPEEVAAT 231  
QY 236 LVGAIENPFLNGEVIRLDGAIIRMG 260  
DB 232 LFLASEBASFTIGAVLPYDGGITAQ 256





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FILING DATE: 13-AUG-1990  
APPLICATION NUMBER: 67,695  
FILING DATE: 29-JUN-1987  
SEQ ID NO: 4  
LENGTH: 273  
5512669-4

Query Match 21.7%; Score 282.5; DB 6; Length 273;  
Best Local Similarity 31.5%; Pred. No. 3,4e-23;  
Matches 90; Conservative 42; Mismatches 91; Indels 63; Gaps 11;

QY 12 VAVITGGASGLATARAERLYVGOGASAVLLDLPNSGGEQAOKKGNVCFAA-----63  
DB 4 VALVVGSGRGIG-----AASIALKAAGYKVAASAYAGNDDAKPKAETGTAV 51  
QY 64 ---DYTSKDVOTALALAKGKRGYDAVAVNCAGIYVASKTYNLKKGTH--TLEDFOHVL 118  
DB 52 YKMDVSYACVEGIAKVAEADLGPIDVLYNNAGIT-----KXAMFHKMTPDQWNV 103  
QY 119 DVNLKGTENVY-----RLV-----AGKMGQ-NEPDGQGR---GVILN 152  
DB 104 NTNLGLFNMTHPYVSGMDRSGFRIVNISSINGQKGMQANYSVSGMDRSGFRIVN 163  
QY 153 TASVAFEGOVGAAYASAKSGIGVGNLTPIARDLAPIGRVTIAPGLFGLTSLPEK 212  
DB 164 ISSINGQKGMQANYSAKKADLGTETKALAEAGAKGTTVAICPGYIGTETMAAIREK 223  
QY 213 VCN-FLASQVPEPSRLGDPAXAHLY--CAITENPFLNGEVIRLDG 255  
DB 224 VLNERIIPQIPV-GRIGEPDEIARIYVELASDEAGITSGTISANG 268

RESULT 18  
US-09-134-001C-4431  
Sequence 4431, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134, 001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064, 964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055, 779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 4431  
LENGTH: 274  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4431

Query Match 21.4%; Score 278.5; DB 4; Length 274;  
Best Local Similarity 31.7%; Pred. No. 9.6e-23;  
Matches 85; Conservative 45; Mismatches 93; Indels 45; Gaps 8;

QY 12 VAVITGGASGLATARAERLYVGOGASAVLLDLP-----NSGGEQAOKKGNVCFA 60  
DB 10 IAVITGASTIGOGASAVALLAEAGAHVLDISQLETVQSIINDNGKATAYRV-----63  
QY 61 APADYVSEKVOYALALAKGKRGYDAVAVNCAGIYVASKTYNLKKGTH--TLEDFOHVL 118  
DB 64 ---DISDDKOVKOFSEKIAOEFHGVYIFENAGVDNGA-----GRHIEYVPEVFDKIM 113  
QY 119 DVNLKGTENVYIRVAGMGONEPDGQGRVITINTASVAFEGOVGAAYASAKSGIGV 178  
DB 114 AVDMRGTELVTKFL-----PLMKKGGSIIINTASFSQADLVRSVYNAKGVIN 166  
QY 179 TLPARDLAPIGRVTIAPGLTSLPEK-----TSLPEKCNLASQ--VPEPSRLGDA 231  
DB 167 TKSIAIEYGRNTRAAIAIETPLVONLAGTSDEAGQTREROKWVTPJRLGTPD 226

QY 232 EYALVQ--AITENPFLNGEVIRLDGAI 257  
DB 227 EVGLVAFILASDDSSFITGETIRIDGV 254

RESULT 19  
US-09-134-001C-4825  
Sequence 4825, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134, 001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064, 964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055, 779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 4825  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4825

Query Match 21.0%; Score 273.5; DB 4; Length 249;  
Best Local Similarity 29.1%; Pred. No. 3e-22;  
Matches 74; Conservative 54; Mismatches 105; Indels 21; Gaps 6;

QY 13 AVITGGASGLATARAERLYVGOGASAVLLDLPNSGGEQA-----KKGNNCVFAPAVTS 67  
DB 10 ALVTGASGIGRSTALAEIGYN-VAVNAGSKDKAEVVEELKAGVESFAIOANYAK 68  
QY 68 EKDVOYALALAKGKRGYDAVAVNCAGIYVASKTYNLKKGTH--TLEDFOHVLNMGTFN 127  
DB 69 GDEVEMKEIYVSGFSDVLYNNAGITKMLMKKE-----QEMDDVIDTMLKGVFN 122  
QY 128 VYRLVAGMGONEPDGQGRVITINTASVAFEGOVGAAYASAKSGIGVMTLPARDIA 187  
DB 123 CLOKVTPLMLKNO-----RSQIILNLISIVGAMGPGQANVYIRKAGVIGLTKAARELA 176  
QY 188 PIGIRVMTIAPGLTSLPEKVCNFIASQVPEPSRLGDPAXAHLYVAIEN--PF 245  
DB 177 SRGITVNAVAPGFIVSDMTNLSDLDKQMLEQIPL-KRFGEDHDIANTVAFILASDRAKY 235  
QY 246 LMGVYIRLDGAI 259  
DB 236 ITGOTIHVNGGTM 249

RESULT 20  
US-09-238-481-2  
Sequence 2, Application US/09238481  
Patent No. 6110704  
GENERAL INFORMATION:  
APPLICANT: Huang, Jianzhong  
APPLICANT: McDevitt, Damien  
TITLE OF INVENTION: FabG  
FILE REFERENCE: GM10192  
CURRENT APPLICATION NUMBER: US/09/238, 481  
CURRENT FILING DATE: 1999-01-28  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 246  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-09-238-481-2

Query Match 20.7%; Score 269.5; DB 3; Length 246;

APPLICATION NUMBER: 08/562,114  
FILING DATE: 22-No. 6280997ember-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/375,962  
FILING DATE: 20-January-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/258,418  
FILING DATE: 10-June-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 628097man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5372.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-8200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase  
US-08-729-594A-13

Query Match 21.9%; Score 285.5; DB 4; Length 244;  
Best Local Similarity 29.6%; Pred. No. 1.3e-23;  
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLVAVITGGASGLIATAEELVGGASAVLIDLPSGSGEQAOKKLGNNCFAPADVTSE 68  
DB 4 EKIALVTGASRGIRAIETLAARGKVIGTATSENGAQAISDYLGNKGKGLMLNVTDP 63  
QY 69 KDQVOTALAKGKFGPRDVAVNAGIAVASKTYNLKKGQHTLLEDFQVLDVNLGTFNY 128  
DB 64 ASIESVLEKIRAEFGEDVILVNNAGITRDNLKMKD-----EEMNDIIEFTNLSVFR 117  
QY 129 IRLVAGENGQNEPDGQGVIIINTASVAFAEGOVQAAYASAKGIVGTLPIARDLAP 188  
DB 118 SKAVRAMMK-----RHGRITIGSVGTGNGGQANVAAKAGIGFSKSLAREVAS 171  
QY 189 IGRVMTIAPGLFGTPLTSLPEKVCNFLASQVPPSRIGDPAEYAHVQ--AIIENPFL 246  
DB 172 RGIIVNVVAPGFIETDTRALSDQRAIGLAQVP-AGRLGGAQELANNAVATLASDEAYI 230  
QY 247 NGEVIRLDGAIRM 259  
DB 231 TGETLHVNGMYM 243

RESULT 16  
US-08-937-993-13

Sequence 13, Application US/08937993  
Patent No. 6399344  
GENERAL INFORMATION:  
APPLICANT: Eriksson, Ulf; Simon, Andras; Romeit, Anna  
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R  
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski L.L.P.  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,993

FILING DATE: September 26, 1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/729,594  
FILING DATE: 11-October-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/562,114  
FILING DATE: 22-No. 6399344ember-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/375,962  
FILING DATE: 20-January-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/258,418  
FILING DATE: 10-June-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6399344man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase  
US-08-937-993-13

Query Match 21.9%; Score 285.5; DB 4; Length 244;  
Best Local Similarity 29.6%; Pred. No. 1.3e-23;  
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLVAVITGGASGLIATAEELVGGASAVLIDLPSGSGEQAOKKLGNNCFAPADVTSE 68  
DB 4 EKIALVTGASRGIRAIETLAARGKVIGTATSENGAQAISDYLGNKGKGLMLNVTDP 63  
QY 69 KDQVOTALAKGKFGPRDVAVNAGIAVASKTYNLKKGQHTLLEDFQVLDVNLGTFNY 128  
DB 64 ASIESVLEKIRAEFGEDVILVNNAGITRDNLKMKD-----EEMNDIIEFTNLSVFR 117  
QY 129 IRLVAGENGQNEPDGQGVIIINTASVAFAEGOVQAAYASAKGIVGTLPIARDLAP 188  
DB 118 SKAVRAMMK-----RHGRITIGSVGTGNGGQANVAAKAGIGFSKSLAREVAS 171  
QY 189 IGRVMTIAPGLFGTPLTSLPEKVCNFLASQVPPSRIGDPAEYAHVQ--AIIENPFL 246  
DB 172 RGIIVNVVAPGFIETDTRALSDQRAIGLAQVP-AGRLGGAQELANNAVATLASDEAYI 230  
QY 247 NGEVIRLDGAIRM 259  
DB 231 TGETLHVNGMYM 243

RESULT 17  
5512669-4

Patent No. 5512669  
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.  
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA  
REDUCTASE

NUMBER OF SEQUENCES: 7  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,667  
FILING DATE: 29-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 124,570  
FILING DATE: 20-SEP-1993  
APPLICATION NUMBER: 944,488  
FILING DATE: 03-NOV-1992  
APPLICATION NUMBER: 566,535



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TYPE: PRF  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4512

Query Match 22.6%; Score 295; DB 4; Length 263;  
Best Local Similarity 32.3%; Pred. No. 1.3e-24;  
Matches 86; Conservative 42; Mismatches 104; Indels 34; Gaps 6;

12 VAVITGASGLTAERLVGOGASAVLLDLPNSGGEAAKLT---GNCCFAPADYSE 68  
11 VAVVVGAGOGIGLTAERLVGOGASAVLLDLPNSGGEAAKLT---GNCCFAPADYSE 70  
69 KDVTALALAKGFRGVAVNCAGIYASAKTYNLKGGOTHTLEDFORVLDVNLGTFNV 128  
71 DQVSVTLNQGVEHGGDLNVLNNAGLGPMTPI-----ESVPEQFNQVGVNAGVFWG 124  
129 IRLVAGMGONPDGOGGQGVIIINTASVAAFEGOVQAAVSASKGIVGMLPIARDLAP 188  
125 IQAALTEQF-----DKLHGKGIINATSOQVGEANGLSYSTKFAVRGLTVAAARDLAE 179  
189 IGRVMTIAPGLFGTPLLTSLEPKVCFNLASQVPEP-----SRLGDPAEYA 234  
180 KNTVNAFAPGIETPEPMKGIAREK---LAENNQPMENMGKQFTDQALAKRLSPEDYA 235  
235 HLVOAIT--ENPFLNGEVRILDGATR 258  
236 NVVSFLAGSDSDYITGTITIVDGMR 261

RESULT 11

US-09-163-189B-6  
Sequence 6, Application US/09363189B  
Patent No. 624228  
GENERAL INFORMATION:  
APPLICANT: SUGIYAMA, MASARAZU  
APPLICANT: TONOUCHI, NAOTO  
APPLICANT: SUZUKI, SHUNICHI  
APPLICANT: YOKOZAKI, KENZO  
TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF  
FILE REFERENCE: 0010-1024-0  
CURRENT APPLICATION NUMBER: US/09/363,189B  
CURRENT FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: JP10-216047  
PRIOR FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patent version 3.0  
SEQ ID NO 6  
LENGTH: 262  
TYPE: PRF  
ORGANISM: Gluconobacter oxydans  
US-09-363-189B-6

Query Match 22.4%; Score 292.5; DB 4; Length 262;  
Best Local Similarity 31.6%; Pred. No. 2.5e-24;  
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

6 RSVKGLVAVITGGASGLTAERLVGOGASAVLLDLPNSG---GEOAKKLGNNCFAP 62  
3 KRFNGKVCIVTGGAGNIGLTAERLVGOGASAVLLDLPNSG---GEOAKKLGNNCFAP 62  
63 ADVTSEKDVOTATLALAKGFRGVAVNCAGIYASAKTYNLKGGOTHTLEDFORVLDVNL 122  
63 CDVTSEKDVOTATLALAKGFRGVAVNCAGIYASAKTYNLKGGOTHTLEDFORVLDVNL 117  
123 MGFNVIRLVAGEM-GONEDDGGQGVIIINTASVAAFEGOVQAAVSASKGIVGMLPI 181  
118 TGAFFHVLKAVSRQMTITN-----YGRIVNTASMGVKGPPMMAAYASGSKAIIALTET 170  
182 IARPLAIGIRVMTIAPGLFGTPLLTSLEPKVCFNLASQVPEP-----SRLGDPAEYA 235  
171 AALDLAAYNIRKVAISPGYMGPGFMEROVLELAKVSGSYFTDPKVVAAQOMIGSVPM-R 229  
226 RLGGPAAEYVHLVOAIT--ENPFLNGEVRILDG 255

Db 230 RYGDINEIPGVAVFLLGDDSSFMGTGVALPIAG 261

RESULT 12  
5229279-7  
Patent No. 5229279  
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.  
TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER  
BIOPOLYMERS  
NUMBER OF SEQUENCES: 8  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/556,535  
FILING DATE: 13-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 67,695  
FILING DATE: 29-AUG-1987  
SEQ ID NO: 7  
LENGTH: 246  
5229279-7

Query Match 22.0%; Score 287.5; DB 6; Length 246;  
Best Local Similarity 31.9%; Pred. No. 8.1e-24;  
Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

12 VAVITGASGLTAERLVGOGASAVLLDLPNSGGE---AQAKKLGNNCFAPADYTS 67  
5 IAYVGGMGIGITAIQRLANGFRVYAGCGSPRREKMLEQKALGFPIASEGNVAD 64  
68 EKDVTALALAKGFRGVAVNCAGIYASAKTYNLKGGOTHTLEDFORVLDVNLGTFN 127  
65 WDKTKIADKXKSEVEVDVILNAGI---TRDVEERK---MTADMDAVIDETLTSLEN 118  
128 VIRLVAGMGONPDGOGGQGVIIINTASVAAFEGOVQAAVSASKGIVGMLPIARDLAP 187  
119 VTKQVIDMA---DRGV--GRIVNISVNGQKQFOGTNTSTAKGLHGTMLAEVA 172  
188 PIGIRVMTIAPGLFGTPLLTSLEPKVCFNLASQVPEPRLDPAEYVHLVOAIT--ENP 245  
173 TKGVAVNVSPGCIATLTDVKAIRQDVLDKIVAITPV-KRGLPGLSISICAMLSSESGF 231  
246 LNGEVRILDGATR 259  
232 STGADFSINGLHM 245

RESULT 13  
US-08-375-962B-13  
Sequence 13, Application US/08375962B  
Patent No. 5731195  
GENERAL INFORMATION:  
APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,  
APPLICANT: CHRISTER, ERIKSSON, ULF.  
TITLE OF INVENTION: Isolated Nucleic Acid Molecule  
TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol  
TITLE OF INVENTION: Delayedrogenase Activity and Which Associates With P63,  
TITLE OF INVENTION: A Portion of a Retinol Binding Protein Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect (ASCII standard)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/375,962B  
FILING DATE: 20-January-1995  
CLASSIFICATION: 435

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/793,035
  FILING DATE: 28-JUL-1997
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: GB 9414622.2
    FILING DATE: 20-JUL-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: GB95/01678
    FILING DATE: 17-JUL-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: Kammerer, Patricia A.
    REGISTRATION NUMBER: 29,775
    REFERENCE/DOCKET NUMBER: MOBT.132
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 713.787.1400
    TELEFAX: 713.787.1440
  INFORMATION FOR SEQ ID NO: 9:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 315 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
US-08-793-035-9
```

```
Query Match      22.7%; Score 296; DB 3; Length 315;
Best Local Similarity 30.9%; Pred. No. 1.4e-24;
Matches 81; Conservative 44; Mismatches 115; Indels 22; Gaps 6;

QY 4 AVRSVGLVAVITGSGSLGATAEPLVVGASAVLLDPRSGGA-----QAKLGNNC 58
DB 66 AVPKVESPVVVVVGASRGIGKAIALSL-GKAGCKVLVNVARSAREBEVSKQIEYVGQA 124
QY 59 VFAPADVTESEKDVQATLALAKGKGRVDVAVNCAGIYASKTYNLKGQTHLEDFORVL 118
DB 125 ITFGGDVSEKADVEAMKMTALIDAMGTIDVVVNNAGITRDITLLIRKKSQ-----WDEV 178
QY 119 DVNLGMTENVIRLVAGEGQNEPDGQGGVITINTASVALEFGVGGQAAYSAKSGIYGM 178
DB 179 DNLGVFLCTQATKIMKK-----RKRITINIASVGLIGNIGQANVAAKAGVIGF 232
QY 179 TLPIADLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHLVQ 238
DB 233 SKTAAEGASRNINNVVCPGFIASDMTAKIGEDMEKTLITGTP-L-GRYGQPEDVAGIVE 291
QY 239 AITENP---FLNGEVIRLDGAI 257
DB 292 FLALSPAASYITGQAFITDGI 313
```

```
RESULT 9
US-08-793-035-10.
Sequence 10, Application US/08793035
Patent No. 6011201
GENERAL INFORMATION:
  APPLICANT: Slabas, Antoni R.
  APPLICANT: White, Andrew
  APPLICANT: Chase, Dianne
  APPLICANT: Elborough, Kelvin
  APPLICANT: Fentem, Phillip A.
  TITLE OF INVENTION: B-ketocacyl ACP Reductase Genes from
  TITLE OF INVENTION: Brassica Napus
  NUMBER OF SEQUENCES: 10
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold White & Durkee
    STREET: P.O. Box 4433
    CITY: Houston
    STATE: TX
    COUNTRY: US
    ZIP: 77210-4433
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/793,035
  FILING DATE: 28-JUL-1997
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: GB 9414622.2
    FILING DATE: 20-JUL-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: GB95/01678
    FILING DATE: 17-JUL-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: Kammerer, Patricia A.
    REGISTRATION NUMBER: 29,775
    REFERENCE/DOCKET NUMBER: MOBT.132
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 713.787.1400
    TELEFAX: 713.787.1440
  INFORMATION FOR SEQ ID NO: 10:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 315 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
US-08-793-035-10
```

```
Query Match      22.7%; Score 296; DB 3; Length 315;
Best Local Similarity 30.9%; Pred. No. 1.4e-24;
Matches 81; Conservative 44; Mismatches 115; Indels 22; Gaps 6;

QY 4 AVRSVGLVAVITGSGSLGATAEPLVVGASAVLLDPRSGGA-----QAKLGNNC 58
DB 66 AVPKVESPVVVVVGASRGIGKAIALSL-GKAGCKVLVNVARSAREBEVSKQIEYVGQA 124
QY 59 VFAPADVTESEKDVQATLALAKGKGRVDVAVNCAGIYASKTYNLKGQTHLEDFORVL 118
DB 125 ITFGGDVSEKADVEAMKMTALIDAMGTIDVVVNNAGITRDITLLIRKKSQ-----WDEV 178
QY 119 DVNLGMTENVIRLVAGEGQNEPDGQGGVITINTASVALEFGVGGQAAYSAKSGIYGM 178
DB 179 DNLGVFLCTQATKIMKK-----RKRITINIASVGLIGNIGQANVAAKAGVIGF 232
QY 179 TLPIADLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHLVQ 238
DB 233 SKTAAEGASRNINNVVCPGFIASDMTAKIGEDMEKTLITGTP-L-GRYGQPEDVAGIVE 291
QY 239 AITENP---FLNGEVIRLDGAI 257
DB 292 FLALSPAASYITGQAFITDGI 313
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RESULT 10
US-09-134-001C-4512
Sequence 4512, Application US/09134001C
Patent No. 6360370
GENERAL INFORMATION:
  APPLICANT: Lynn Doucette-Stamm et al
  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
  TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
  FILE REFERENCE: GTC-007
  CURRENT APPLICATION NUMBER: US/09/134,001C
  PRIOR FILING DATE: 1998-08-13
  PRIOR APPLICATION NUMBER: US 60/064,964
  PRIOR FILING DATE: 1997-11-08
  PRIOR APPLICATION NUMBER: US 60/055,779
  PRIOR FILING DATE: 1997-08-14
  NUMBER OF SEQ ID NOS: 5674
  SEQ ID NO 4512
  LENGTH: 263
```

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NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/815,225  
FILING DATE: 12-MAR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/55209  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-815-225-4

Query Match 23.0%; Score 300; DB 4; Length 255;  
Best Local Similarity 33.2%; Pred. No. 3,5e-25;  
Matches 85; Conservative 48; Mismatches 103; Indels 20; Gaps 8;

QY 5 VRSVGLVAVITGASGIGLTAERLVGQASAVLLDLPNSGSGRAOKKLNCCVFAPAD 64  
DB 1 MNDLSKRTYITGARGIGLAEARQAARVAVLADVLDEGATATLGDPAAYCHLD 60  
QY 65 VTSEKDVOTALAKGRGRVDVAVNCAGIAVASTYMLKKQCTHTLDFQRYLDVNLG 124  
DB 61 VVEEDMORVAVYAAEEFSGVDGLVNNAGISTGMFL-----ETESVERFRVVDINLTG 114  
QY 125 TENVIRLVAGMGQNEPDGQGRVYIINTASVAAFEGQVQAAYSASKGIYGMTLPAR 184  
DB 115 VETGKMTVTPAK-----KDAAG--GSLVINSSAAGLMGLATSSYASKMGVAGLSKLAAY 168  
QY 185 DLAPIGIRVMTIAPGLFGTPLL--TSLPEKVCNFIASQVPPFSRIG-DPAFAHLYQAI 241  
DB 169 ELGTDRIKRVNSVHPGRTYTPMTAETGIRGEGNY--PMTIPM-GRVGNBEGELAGAVVKLL 225  
QY 242 E--NPLNGEIVRLDG 255  
DB 226 SDTSSVTGAGLAVID 241

RESULT 7  
US-08-440-856A-4  
Sequence 4, Application US/08440856A  
Patent No. 5750873  
GENERAL INFORMATION:  
APPLICANT: DELLAPORTA, STEPHEN L.  
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING  
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 2000 PENNSYLVANIA AVE. N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA

ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,856A  
FILING DATE: 15-MAY-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A.  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 05463-20001.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1517  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 333 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-440-856A-4

Query Match 23.0%; Score 299.5; DB 1; Length 333;  
Best Local Similarity 32.5%; Pred. No. 6,1e-25;  
Matches 92; Conservative 46; Mismatches 106; Indels 39; Gaps 5;

QY 6 RSVKGLVAVITGASGIGLTAERLVGQASAVLLDLPNSGSGRAOKKLNCCVFAPAD 65  
DB 50 KRLGKVAIVTGGARGIGLAEARQAARVAVLADVLDEGATATLGDPAAYCHLD 109  
QY 66 TSEKDVOTALAKGRGRVDVAVNCAGIAVASTYMLKKQCTHTLDFQRYLDVNLG 125  
DB 110 SVEDVRAVRAVYARIGRDVLCNNAGV-LGRTQRAKSLISFDGGEFDRVAVNAGA 168  
QY 126 FNVIRLVAGMGQNEPDGQGRVYIINTASVAAFEGQVQAAYSASKGIYGMTLPAR 185  
DB 169 ALGKHAALMTOR-----FAGSIISVAVAGVLGPHAYTASKHAIVGLTKNAEE 222  
QY 186 LAPGIRVMTIAPGLFGTPLL-----TSLP-----EKYC 214  
DB 223 LGAGIRVNCISPPGATVPHLINARQGHASTADADADIDIDIAVPSQGEVKEKBEVY 282  
QY 215 NFASQVPPFSRIGDPAEYAHLYQAIENPFLNGEIVRLDGAI 257  
DB 283 RGLATLKGATLRPRDIAE-AALFLASDSRYISGHNLYVDGCV 324

RESULT 8  
US-08-793-035-9  
Sequence 9, Application US/08793035  
Patent No. 6011201  
GENERAL INFORMATION:  
APPLICANT: Slabas, Antoni R.  
APPLICANT: White, Andrew  
APPLICANT: Chase, Dianne  
APPLICANT: Elborough, Keiran  
APPLICANT: Fentem, Phillip A.  
TITLE OF INVENTION: B-Ketocacyl ACP Reductase Genes From  
TITLE OF INVENTION: Brassica Napus  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

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Page 3

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES  
FILE REFERENCE: 25885-1651  
CURRENT APPLICATION NUMBER: US/09/347, 878C  
CURRENT FILING DATE: 1999-07-06  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 50  
LENGTH: 261  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-347-878-50

Query Match 99.68; Score 1299; DB 4; Length 261;  
Best Local Similarity 99.68; Pred. No. 4,3e-136;  
Matches 260; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAAVRSYKGLAVITGASGLGATATERTLVGASAVLLDLPNSGGEAQAQKLNCCVF 60  
DB 1 MAAACRSYKGLAVITGASGLGATATERTLVGASAVLLDLPNSGGEAQAQKLNCCVF 60  
OY 61 APADVTSEKDVOTATLAKGKFRGVDAVNCAGIAVASKTYNKKGGTHLEDFQRLDV 120  
DB 61 APADVTSEKDVOTATLAKGKFRGVDAVNCAGIAVASKTYNKKGGTHLEDFQRLDV 120  
OY 121 NLMGFENVIRLVAGEMGONEPDGOGORVINTASVAFEQGVQAAYASAKSGIVGML 180  
DB 121 NLMGFENVIRLVAGEMGONEPDGOGORVINTASVAFEQGVQAAYASAKSGIVGML 180  
OY 181 PIARDLADIGIRVMTIAPGLFTPLTSLPEKVCNFTLASOVPPPSRLGDPAYAHVQAI 240  
DB 181 PIARDLADIGIRVMTIAPGLFTPLTSLPEKVCNFTLASOVPPPSRLGDPAYAHVQAI 240  
OY 241 IENPFLNGEVRILDGAIRMOP 261  
DB 241 IENPFLNGEVRILDGAIRMOP 261

RESULT 4  
US-08-980-832-41  
Sequence 41, Application US/08980832B  
Patent No. 6291204  
GENERAL INFORMATION:  
APPLICANT: Pasamontes, Luis  
APPLICANT: Tsysanukov, Yuri  
TITLE OF INVENTION: Improved Fermentative Carotenoid Production  
FILE REFERENCE: Improved Fermentative Carotenoid  
CURRENT APPLICATION NUMBER: US/08/980,832B  
CURRENT FILING DATE: 1997-12-01  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 388  
TYPE: PRT  
ORGANISM: Flavobacterium sp. R1534  
US-08-980-832-41

Query Match 51.0%; Score 664.5; DB 4; Length 388;  
Best Local Similarity 55.5%; Pred. No. 2,3e-65;  
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

OY 8 VEGIVAVITGASGLGATATERTLVGASAVLLDLPNSGGEAQAQKLNCCVFAPADYTS 67  
DB 143 IGRVYVVYTGASGLGASARMLAOGAKVVLADL-----AEPKDAPEGAVHAACDVT 196  
OY 68 EKDVOATLALAKGKFRGVDAVNCAGIAVASKTYNKKGGTHLEDFQRLDVNLGTFN 127  
DB 197 ATAAQTAIALADRFRLDGLVNCAGIAFAERM--LGRGPRGLDSFAFAVAINIGSFN 254  
OY 128 VIRLVAGEMGONEPDGOGORVINTASVAFEQGVQAAYASAKSGIVGMLPIARDLA 187  
DB 255 MARLAEMAKRNPV-GERGVIVNTASIAADGQIGQVAYASAKSGIVGMLPIARDLA 313  
OY 188 PIGIRVMTIAPGLFTPLTSLPEKVCNFTLASOVPPPSRLGDPAYAHVQAIENPFLN 247

DB 314 RHGIRVMTIAPGLFTPLTSLPEKVCNFTLASOVPPPSRLGDPAYAHVQAIENPFLN 373  
OY 248 GEYIRLDGAIRMOP 261  
DB 374 GEYIRLDGAIRMOP 387

RESULT 5  
US-09-239-052-2  
Sequence 2, Application US/09239052  
Patent No. 6346395  
GENERAL INFORMATION:  
APPLICANT: Holmes, David J.  
APPLICANT: Zhong, Yiyi  
APPLICANT: Debouck, Christine  
APPLICANT: Jaworski, Deborah D.  
APPLICANT: Wang, Min  
APPLICANT: Warren, Richard L.  
APPLICANT: McDevitt, Daniel  
APPLICANT: Kosmatka, Anna L.  
APPLICANT: Ingraham, Karen A.  
APPLICANT: Chalke, Alison F.  
APPLICANT: So, Chi Young  
APPLICANT: Wallis, Nicola G.  
APPLICANT: Pearson, Stewart C.  
TITLE OF INVENTION: FabG  
FILE REFERENCE: GM10191  
CURRENT APPLICATION NUMBER: US/09/239, 052  
CURRENT FILING DATE: 1999-01-27  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-09-239-052-2

Query Match 25.0%; Score 326.5; DB 4; Length 243;  
Best Local Similarity 35.1%; Pred. No. 3,7e-28;  
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

OY 15 ITGASGLGATATERTLVGASAVLLDLPNSGGE-----AQAKKLNCCVFAPADYTS 68  
DB 10 ITGSSRSIGLAIHAKFQAQANIVL-----NSRGAISLELAHSNGIKVPSISGVSDR 65  
OY 69 KDVOATLALAKGKFRGVDAVNCAGIAVASKTYNKKGGTHLEDFQRLDVNLGTFN 128  
DB 66 ADARIMIDQAIELGSDVAVNNAGI--TQDTMLAKV---TEADEKVKVNLGAFNM 119  
OY 129 IRLVAGEMGONEPDGOGORVINTASVAFEQGVQAAYASAKSGIVGMLPIARDLA 188  
DB 120 TQSVL-----KPMKARREGATIMSSVGLMGVIGQANTAAKAGLIGTRKSVAREVAS 173  
OY 189 IGRVMTIAPGLFTPLTSLPEKVCNFTLASOVPPPSRLGDPAYAHVQAIENPFLN 248  
DB 174 RNIRVNTIAPGLMISDMTALISDKIKATLAQIPM--KEFGAEGVADLFTVLAGODYLTG 232  
OY 249 EYIRLDGAIRM 259  
DB 233 QVIAIDGGLSM 243

RESULT 6  
US-08-815-225-4  
Sequence 4, Application US/08815225  
Patent No. 6268479  
GENERAL INFORMATION:  
APPLICANT: Stern, David M.  
APPLICANT: Yan, Shi Du  
TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE  
BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING  
NEURODEGENERATIVE CONDITIONS

## ALIGNMENTS

## RESULT 1

US-08-815-225-2

Sequence 2, Application US/08815225

Patent No. 6268479

GENERAL INFORMATION:

APPLICANT: Stern, David M.

APPLICANT: Yan, Shi Du

TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cooper &amp; Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,225

FILING DATE: 12-MAR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/55209

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 391-0525

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ. ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-815-225-2

Query Match 99.6%; Score 1299; DB 4; Length 261;  
Best Local Similarity 99.6%; Pred. No. 4.3e-136;  
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAAVSVKGLVAVITGASGLGLATAERLVGGASAVLLDLPNSGGEAQAARKLGNNCF 60  
DB 1 MAAACRSVKGIVAVITGASGLGLATAERLVGGASAVLLDLPNSGGEAQAARKLGNNCF 60  
QY 61 APADVTSKDVQOTALALAKGKFGVDVAVNAGIAVASKTYNKKGTHTLEDFORVLDV 120  
DB 61 APADVTSKDVQOTALALAKGKFGVDVAVNAGIAVASKTYNKKGTHTLEDFORVLDV 120  
QY 121 NLMGTFNIVRLVAGMGONEDPDGQGRVINTASVAAFEGVGOAAVSASKGGIVGML 180  
DB 121 NLMGTFNIVRLVAGMGONEDPDGQGRVINTASVAAFEGVGOAAVSASKGGIVGML 180  
QY 181 PIARDLAPIGIRVMTIAPGLTGLTSLPERKVCNFLASQVPPSRSLGDPAEVAHLVOAI 240  
DB 181 PIARDLAPIGIRVMTIAPGLTGLTSLPERKVCNFLASQVPPSRSLGDPAEVAHLVOAI 240  
QY 241 IENPFLNGEVIRLDGAIRMP 261  
DB 241 IENPFLNGEVIRLDGAIRMP 261

US-08-815-225-3

Sequence 3, Application US/08815225

Patent No. 6268479

GENERAL INFORMATION:

APPLICANT: Stern, David M.

APPLICANT: Yan, Shi Du

TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cooper &amp; Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,225

FILING DATE: 12-MAR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/55209

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 391-0525

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ. ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-815-225-3

Query Match 99.6%; Score 1299; DB 4; Length 261;  
Best Local Similarity 99.6%; Pred. No. 4.3e-136;  
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAAVSVKGLVAVITGASGLGLATAERLVGGASAVLLDLPNSGGEAQAARKLGNNCF 60  
DB 1 MAAACRSVKGIVAVITGASGLGLATAERLVGGASAVLLDLPNSGGEAQAARKLGNNCF 60  
QY 61 APADVTSKDVQOTALALAKGKFGVDVAVNAGIAVASKTYNKKGTHTLEDFORVLDV 120  
DB 61 APADVTSKDVQOTALALAKGKFGVDVAVNAGIAVASKTYNKKGTHTLEDFORVLDV 120  
QY 121 NLMGTFNIVRLVAGMGONEDPDGQGRVINTASVAAFEGVGOAAVSASKGGIVGML 180  
DB 121 NLMGTFNIVRLVAGMGONEDPDGQGRVINTASVAAFEGVGOAAVSASKGGIVGML 180  
QY 181 PIARDLAPIGIRVMTIAPGLTGLTSLPERKVCNFLASQVPPSRSLGDPAEVAHLVOAI 240  
DB 181 PIARDLAPIGIRVMTIAPGLTGLTSLPERKVCNFLASQVPPSRSLGDPAEVAHLVOAI 240  
QY 241 IENPFLNGEVIRLDGAIRMP 261  
DB 241 IENPFLNGEVIRLDGAIRMP 261

RESULT 3  
US-09-347-878-50  
Sequence 50, Application US/09347878C  
Patent No. 6376210  
GENERAL INFORMATION:



Thu Jun 26 06:55:07 2003

us-09-931-186-4.ra1

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 14:24:27 ; Search time 12.1667 Seconds  
(without alignments)  
631.182 Million cell updates/sec

Title: US-09-931-186-4  
Perfect score: 1304  
Sequence: 1 MAAVRSKGLAVITIGAS.....ENFLNGEYIRLDGAIKMP 261

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: /cgn2\_6/ptodata/1/aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1299	99.6	261	4	US-08-815-225-2
2	1299	99.6	261	4	US-08-815-225-3
3	1299	99.6	261	4	US-09-347-878-50
4	664.5	51.0	388	4	US-08-980-832-41
5	326.5	25.0	243	4	US-09-239-052-2
6	300	23.0	255	4	US-08-815-225-4
7	299.5	23.0	333	1	US-08-440-856A-4
8	296	22.7	315	3	US-08-793-035-9
9	296	22.7	315	3	US-08-793-035-10
10	295	22.4	263	4	US-09-134-001C-4512
11	292.5	22.4	262	4	US-09-363-189B-6
12	287.5	22.0	246	6	5229279-7
13	285.5	22.0	244	1	US-08-375-962B-13
14	285.5	21.9	244	2	US-08-562-114B-13
15	285.5	21.9	244	4	US-08-729-594A-13
16	285.5	21.9	244	4	US-08-937-993-13
17	282.5	21.7	273	6	5512669-4
18	278.5	21.4	274	4	US-09-134-001C-4431
19	273.5	21.0	249	4	US-09-134-001C-4825
20	269.5	20.7	246	3	US-09-238-881-2
21	269.5	20.7	246	4	US-09-572-810A-2
22	269	20.6	246	4	US-09-134-001C-4397
23	268	20.6	166	4	US-08-858-207A-270
24	267.5	20.5	337	1	US-08-440-856A-3
25	266	20.4	256	4	US-09-504-358-14
26	266	20.4	256	4	US-09-954-314-14
27	264	20.2	247	1	US-08-241-766-13
28	255.5	19.6	263	6	5229279-4
29	254	19.5	261	4	US-09-468-738A-29
30	254	19.5	261	4	US-09-940-019-29
31	252.5	19.4	257	4	US-09-134-001C-3562
32	252.5	19.4	263	4	US-09-134-001C-3505
33	249.5	19.1	252	3	US-08-822-322-8
34	249.5	19.1	252	3	US-08-822-322-9
35	245	18.8	256	1	US-08-594-808B-7
36	243	18.6	271	2	US-07-637-865-2
37	242	18.6	359	1	US-08-440-856A-8
38	238	18.3	258	4	US-09-504-358-12
39	238	18.3	258	4	US-09-954-314-12
40	238	18.3	292	3	US-09-109-205-2
41	238	18.3	292	4	US-09-443-184-58
42	228.5	17.5	231	3	US-08-822-322-9
43	228.5	17.5	231	3	US-08-822-322-9
44	223	17.1	283	4	US-09-367-012-1
45	223	17.1	283	4	US-09-777-157A-1
46	214	16.4	287	4	US-09-134-001C-5042
47	211	16.2	283	4	US-09-134-001C-5346
48	206	15.8	290	4	US-09-134-001C-4339
49	206	15.8	313	4	US-09-413-814-9
50	204	15.6	244	2	US-09-900-567-2
51	204	15.6	248	4	US-09-385-028-11
52	185.5	14.5	295	3	US-09-002-298-5
53	184.5	14.2	292	4	US-09-468-738A-2
54	184.5	14.1	292	4	US-09-940-019-2
55	184.5	14.1	296	4	US-09-468-738A-23
56	184.5	14.1	296	4	US-09-940-019-23
57	184.5	14.1	318	4	US-08-729-594A-39
58	184.5	14.1	318	4	US-08-937-993-39
59	184	14.1	244	1	US-08-762-129-4
60	182.5	14.0	272	4	US-09-134-001C-2864
61	182.5	14.0	295	4	US-09-134-001C-4059
62	182	14.0	244	1	US-08-762-129-3
63	182	14.0	257	4	US-09-287-097-2
64	182	14.0	295	4	US-09-026-482B-2
65	181.5	13.9	318	2	US-08-562-114B-15
66	181.5	13.9	318	3	US-09-109-205-11
67	181.5	13.9	318	4	US-08-729-594A-15
68	181.5	13.9	318	4	US-09-880-427-1
69	181.5	13.9	318	4	US-09-306-538B-1
70	181.5	13.9	318	4	US-08-937-993-15
71	179.5	13.8	318	1	US-08-375-962B-14
72	179.5	13.8	318	4	US-08-940-424-3
73	175	13.4	318	4	US-08-729-594A-38
74	175	13.4	318	4	US-08-937-993-38
75	172	13.2	301	4	US-09-288-143-98
76	172	13.2	303	3	US-09-002-298-1
77	171.5	13.2	244	1	US-08-762-129-1
78	167.5	12.8	317	4	US-08-729-594A-37
79	167.5	12.8	317	4	US-08-937-993-37
80	162	12.4	255	4	US-09-036-987A-21
81	162	12.4	255	4	US-09-370-700-21
82	161.5	12.4	319	2	US-08-977-847-1
83	161.5	12.4	319	2	US-09-195-021-1
84	160.5	12.3	317	3	US-09-109-205-18
85	160.5	12.3	317	4	US-08-940-424-5
86	160.5	12.3	360	4	US-09-740-028A-2
87	159.5	12.2	318	4	US-09-740-028A-4
88	158.5	12.2	318	4	US-08-940-424-2
89	157.5	12.1	316	4	US-08-729-594A-36
90	157.5	12.1	316	4	US-08-937-993-36
91	156.5	12.0	335	3	US-09-002-298-7
92	153.5	11.8	335	3	US-08-977-847-3
93	153.5	11.7	317	2	US-09-195-021-3
94	152.5	11.7	317	4	US-08-940-424-2
95	152.5	11.7	317	4	US-09-109-205-19
96	151.5	11.6	327	3	US-08-375-962B-12
97	151	11.6	327	2	US-08-562-114B-12
98	151	11.6	327	2	US-08-729-594A-12
99	151	11.6	327	4	US-08-937-993-12
100	151	11.6	327	4	US-08-937-993-12

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FT      /note="alpha helix region A"
FT      190..196
FT      Region
FT      /note="beta sheet region F"
FT      204..218
FT      Region
FT      /note="alpha helix region F"
FT      247..252
FT      /note="beta sheet region G"
XX      MO9954347-A2.
XX      28-OCT-1999.
XX      19-APR-1999; 99MO-EP02610.
XX      17-APR-1998; 98US-0082257.
XX      (HORM-) INST HORMON & FORTPFLANZUNGSFORSCHUNG GM.
XX      PI Iwells R, Spiess A, Balvers M, Jaehner D, Hansis C;
XX      WPI; 2000-052699/04.
XX      DR N-PSDB; AA234663.
XX      PT Novel differential display reverse transcription PCR method used to
XX      detect genes expressed in mutant tissues
XX      Claim 4; Fig 2; 40pp; English.
XX      This sequence represents murine Alzheimer-associated beta-amyloid
XX      binding protein (ERAB, see AA332339), a novel member of the SCAD
XX      (short chain alcohol dehydrogenase) family of steroid metabolising
XX      and related enzymes. The sequence was deduced from cDNA (see
XX      AA344663) identified using a novel differential display RT-PCR method
XX      for analysis of w/w mouse testis gene products. ERAB is
XX      specifically upregulated in the testicular Leydig cells of w/w
XX      azoospermic mutant mice, suggesting an important role in the
XX      establishment and support of spermatogenesis. The invention also
XX      relates to vectors, host cells, methods for expressing the ERAB
XX      nucleic acid, and antibodies. The nucleic acid and protein are
XX      useful e.g. as markers for testicular development.
XX      Sequence 260 AA:
XX      Query Match 88.38; Score 1152; DB 21; Length 260;
XX      Best Local Similarity 88.08; Pred. No. 6.6e-105;
XX      Matches 227; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
QY      4 ACRSVKGVAVITGASGLATTAERLVGGASAVLADLPSNGGEAOKKLGNNCFAPA 63
DB      3 AVRSYKGLVAVITGASGLGATATKRLVGGATVLDVDSSENAKKLGESCIFAPA 62
QY      64 DVTSEKDVQALALAKRGFRVDVAVNCAGIYASAKTYNKKGTHTLEDFQRYLVNLM 123
DB      63 NVTSEKQALTLAKRFRIDVAVNCAGIYAVIKTYHKKKNIHTLEDFQRYLVNLI 122
QY      124 GFNVIRLVAGEMQNEPDGSGRGVLIINTASVAFGGVQQAAYSSKGGIVMTPIA 183
DB      123 GFNVIRLVAGEMQNEPDGSGRGVLIINTASVAFGGVQQAAYSSKGGIVMTPIA 182
QY      184 RDLAPGIGIRVMTIPGLTSLPEKVNFLASGVPPSRLDPAEYVAHLVQATIEEN 243
DB      183 RDLAPGIRVMTIPGLTSLPEKVNFLASGVPPSRLDPAEYVAHLVQATIEEN 242
QY      244 PFLNGEVRRLDGAIRMP 261
DB      243 PFLNGEVRRLDGAIRMP 260
XX      RESULT 3
XX      AAM67934
XX      ID AAM67934 standard; 227 AA.
XX      AC AAM67934;

```

CC (see AAX00611 for described uses).

XX Sequence 227 AA:

Query Match 86.9%; Score 1134; DB 20; Length 227;

Best Local Similarity 99.6%; Pred. No. 3.2e-103;

Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAYLDLPNSGSGAQAQKLGNNCVPADVTSEKVVQRLALAKKFGRVDAVAVACAGI 94

DB 1 ASAYLDLPNSGSGAQAQKLGNNCVPADVTSEKVVQRLALAKKFGRVDAVAVACAGI 60

QY 95 AVASKTYNLKKGQHTHTEDFORVLDVNLMTGFNVIRLVAGEMGNPDGQGGRGVLIINTA 154

DB 61 AVASKTYNLKKGQHTHTEDFORVLDVNLMTGFNVIRLVAGEMGNPDGQGGRGVLIINTA 120

QY 155 SVAAFEGQVGAAYASASAKGIVGKTLPIARDLAPIGIRVKTAPGLFGPPLTSLPEKYR 214

DB 121 SVAAFEGQVGAAYASASAKGIVGKTLPIARDLAPIGIRVKTAPGLFGPPLTSLPEKYR 180

QY 215 NPLASQVPEPSRLGDPAPAYAHVQAITEENPFLNGEVRIDGAIKMP 261

DB 181 NPLASQVPEPSRLGDPAPAYAHVQAITEENPFLNGEVRIDGAIKMP 227

RESULT 4

ABB62988 ID ABB62988 standard; Protein: 255 AA.

AC ABB62988;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 15756.

KW Drosophila: developmental biology; cell signalling; insecticide; pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

PI WPI; 2001-656860/75.

DR N-PSDB; ABL07091.

PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

PS interactions -

PS Disclosure; SEQ ID NO 15756; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABLU6176-ABU30511), expressed DNA

CC sequences (ABLU1840-ABLU16175) and the encoded proteins

CC (ABBS7737-ABBS7072).

CC The sequence data for this patent did not form part of the printed

CC specification and was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 255 AA:

Query Match 70.2%; Score 916; DB 22; Length 255;

Best Local Similarity 69.3%; Pred. No. 1e-61; Indels 0; Gaps 0;

Matches 176; Conservative 29; Mismatches 49;

QY 8 VGLVAVITGGASGIGLTAERLVGOGASAVLLDLPNSGSGAQAQKLGNNCVPADVTS 67

DB 2 IKNVSLVTGGASGIGLTAERLVGOGASAVLLDLPNSGSGAQAQKLGNNCVPADVTS 61

QY 68 EKDVQVTLALAKKRGKRVDAVAVNCAGIIVASKITNKKGQHTHTEDFORVLDVNLMTGFN 127

DB 62 EKDVSAALQTLAKDKFGRDLTVNCAGTATVAKTFENFNVAHRLDFORVLTINTVGFEN 121

QY 128 VIRLVAGEMGNPDGQGGRGVLIINTASVAAFEQVGAAYASASAKGIVGKTLPIARDLA 187

DB 122 VIRLVAGEMGNPDGQGGRGVLIINTASVAAFEQVGAAYASASAKGIVGKTLPIARDLS 181

QY 188 PIGIRVMTAPGLFESTPLTSLPEKYRNFASQVPEPSRLGDPAPAYAHVQAITEENPFLN 247

DB 182 TQIRICTIAPGLFESTPLTSLPEKYRNFASQVPEPSRLGDPAPAYAHVQAITEENPFLN 241

QY 248 GEVIRIDGAIKMP 261

DB 242 GEVIRIDGAIKMP 255

RESULT 5

AAM06513 ID AAM06513 standard; Protein: 388 AA.

AC AAM06513;

DT 08-MAR-1997 (first entry)

DE Flavobacterium ORF-5 gene product.

KW Carotenoid; lycopen; beta-carotene; echinenone; canthaxanthin;

KW zeaxanthin; adonixanthin; astaxanthin.

OS Flavobacterium sp. R1534 WT (ATCC 21386).

PN EP747483-A2.

PD 11-DEC-1996.

PF 29-MAY-1996; 96EP-0108556.

PR 09-JUN-1995; 95EP-0108888.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Hohmann H, Pasamontes L, Tessier M, Van Loon A;

PI WPI; 1997-023160/03.

DR N-PSDB; AAT45143.

PT Flavobacterium gene sequences encoding carotenoid biosynthesis

PT enzymes - for the production of carotenoid(s), useful in foods and

PS animal feeds

PS Example 2: Fig 7; 80pp; English.

CC A polypeptide (AAM06513) showing approx. 30% homology to

CC streptomycete polyketide synthases was identified as the product

CC of ORF-5 from a carotenoid gene cluster (see also AAT45143) of

CC Flavobacterium sp. R1534. 5 Other open reading frames of the

CC gene cluster coded for carotenoid biosynthetic enzymes (see also

CC AAM06515-18 and AAM00871) and can be used to produce carotenoids in

CC transformed host cells.

CC Sequence 388 AA;

Query Match 51.2%; Score 668.5; DB 18; Length 388;  
 Best Local Similarity 55.5%; Pred. No. 3.7e-57;  
 Matches 141; Conservative 36; Mismatches 68; Indels 9; Gaps 3;

QY 8 VKGLVAVITGASGLGLATAEERLVGOGASAVLLDLPNSGGEAQARKLGNNCFAPADYTS 67  
 DB 143 IESRIVVVTGAASGLGASABMLAQGAAVVLADL-----APKDAPEGVAHAACDVTD 196  
 QY 68 EKDVQALALAKKFERVDVAVNACGIAVASKTYNKKQGTHTLEDFQVLDVNLMGTFN 127  
 DB 197 AFAQTAIALATDFRFDGLVNCAGIAPRERK--LGRDGPGLDSFARAIVTNLIGSFN 254  
 QY 128 VIRLVAGEMQNEPDGQGRGVIIINTASVAEFGVGOAAYSASKGGIVGMLPIARDLA 187  
 DB 255 MARLAELAMARNPEPR-GERGVIVNTASIAADGGIGQVAYASKAGVAGMTELPMAKDIA 313  
 QY 188 PIGIRVMTAPGLFGTPIPLTSLPEKYRNFLASQVPPPSRLGDPAEYAHVQAIIENPFNL 247  
 DB 314 RGIIRVMTAPGLFGTPIPLTSLPEKYRNFLASQVPPPSRLGDPAEYAHVQAIIENPFNL 373  
 QY 248 GEVIRLDGAIKMP 261  
 DB 374 GEVIRLDGAIKMP 387

## RESULT 6

ABP28011  
 ID ABP28011 standard; Protein; 244 AA.

XX AC ABP28011;

XX DT 02-JUL-2002 (first entry)

XX DE Streptococcus polypeptide SEQ ID NO 5198.

XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;  
 XX antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS Streptococcus agalactiae.

XX PN WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026333.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX PA (CHIR-) CHIRON SPA.

XX PA (GENO-) INST GENOMIC RES.

XX PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

XX PI Tettelin H;

XX DR WPI: 2002-352536/38.

XX PS N-PSDB; ABN68642.

XX PS Claim 1; Page 3863; 4525pp; English.

CC The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins.

XX SQ Sequence 244 AA;

Query Match 28.0%; Score 365.5; DB 23; Length 244;  
 Best Local Similarity 36.5%; Pred. No. 1.2e-27;  
 Matches 92; Conservative 39; Mismatches 98; Indels 23; Gaps 5;

QY 15 ITGSGSGIATAEERLVGOGASAVLLDLPNSGGE-----AQARKLGNNCFAPADYTS 68  
 DB 10 ITGSSRGIGLAIHAQFAQLGANIYL-----NGRSEI SEDLIEFPADYGVKVAISGDVSSF 65  
 QY 69 KDVOITALALAKKFGFRVDVAVNACGIAVASKTYNKKQGTHTLEDFQVLDVNLMGTFN 128  
 DB 66 EDANRMIKEALIASISGVLDVYNAGIT-----NDKLMKMTVEDFESVLKINLTGARFN 119  
 QY 129 IRLVAGEMQNEPDGQGRGVIIINTASVAEFGVGOAAYSASKGGIVGMLPIARDLA 188  
 DB 120 TQSVL-----KPMTKARQGAIIINISVGLTGNVGOANYASKAGLIGFTKSVAREVAA 173

QY 189 IGRVMTAPGLFGTPIPLTSLPEKYRNFLASQVPPPSRLGDPAEYAHVQAIIENPFNL 248  
 DB 174 RGIIRVMTAPGLFGTPIPLTSLPEKYRNFLASQVPPPSRLGDPAEYAHVQAIIENPFNL 232

QY 249 EVIRLDGAIKMP 260

DB 233 OVTAIDGGMTO 244

## RESULT 7

ABP27345  
 ID ABP27345 standard; Protein; 243 AA.

XX AC ABP27345;

XX DT 02-JUL-2002 (first entry)

XX DE Streptococcus polypeptide SEQ ID NO 3866.

XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;  
 XX antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS Streptococcus pyogenes.

XX PN WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026333.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX PA (CHIR-) CHIRON SPA.

XX PA (GENO-) INST GENOMIC RES.

XX PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

XX PI Tettelin H;

XX DR WPI: 2002-352536/38.

XX PS N-PSDB; ABN67976.



Thu Jun 26 06:55:01 2003

us-09-931-186-2.rag

Page 7

XX Streptococcus pneumoniae.  
OS  
XX  
XX W0200044885-41.  
XX  
XX 03-AUG-2000.  
XX  
XX PD  
XX 19-JAN-2000; 2000WO-US01131.  
XX  
XX PF  
XX 27-JAN-1999; 99US-0239052.  
XX  
XX PR  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX PA  
XX Holmes DJ, Mooney J, Zhong YY, Debouck C, Jaworski DD, Wang M;  
PI Warren RL, Kosmatka AB, McDevitt D, Ingraham KA, Chalker AF;  
PI So CY, Wallis NG, Pearson SC;  
XX  
XX  
XX WPI; 2000-482971/42.  
XX  
XX DR  
XX N-PSDB; AAA74684.  
XX  
XX  
XX Fabg polypeptide, isolated from Streptococcus pneumoniae, is used to  
PT treat microbial diseases, identify agonists and antagonists for  
PT treating microbial infections and to detect diseases associated with  
PT microbial infections -  
XX  
XX Claim 1; Page 3; 40pp; English.

CC The present sequence is a Fabg (2-oxoacyl-acyl carrier protein  
CC (reductase) polypeptide. A full length Fabg gene was isolated from a  
CC *Streptococcus pneumoniae* 010093 DNA library in *E. coli*. Fabg  
CC polynucleotides and polypeptides are used for detection and treatment of  
CC microbial diseases. They may also be used to identify antagonists and  
CC agonists which can then be used to treat microbial diseases. Compounds  
CC that interfere with the initial physical interaction between a pathogen  
CC and a host have been identified. The compounds are able to prevent the  
CC adhesion of bacteria to mammalian extracellular proteins in wounds,  
CC prevent adhesion between mammalian extracellular proteins and bacteria  
CC Fabg proteins which mediate tissue damage and/or to block normal  
CC progression of pathogenesis in infections mediated by implantation of  
CC in-dwelling devices or other surgical techniques. The Fabg  
CC polypeptides, polynucleotides, antagonists and agonists are especially  
CC useful in the treatment of *Helicobacter pylori* infection. They may be  
CC used to decrease *H. pylori*-induced cancers and to prevent, inhibit  
CC and/or cure gastric ulcers and gastritis.

Query Match	25.48;	Score	331.5;	DB	21;	Length	243;
Best Local Similarity	35.18;	Pred. No.	2.5e-24;				
Matches	88;	Conservative	37;	Mismatches	103;	Indels	23;
						Gaps	6;

```

QY 15 ITGAGAGGLTAARAEPLVGGASAVYLDLPNSGGE-----AOAKKLGNVCYFAPADVTSE 68
Db 10 ITSSSRKIGTALAHKRAQGANIVL-----NSGAISEBLLAFPSNYGKIVPISGDVSD 65
QY 69 KDVOYATALAKKFGHVDVAVNCGAIVAAKSTYNIKKQOHTLEDFOBYLDVNIKGTENV 128
Db 66 ADKRMIDQAIALGVSVDVLVNNAGI--TODILMKM---TEADFEKVLVNTLGFNM 119
QY 129 IRLVAGMGQNEEDQGGRGVITINNTASVAAFEGGVGOAASASKSGIYGMTLPARDLAP 188
Db 120 TQSVL-----KPMKARFEGAILINSSVYGLMGNTIGQANYAASRAGLIGFKSARREVAS 173
QY 189 IGRVMTIABGLFETDLTSLPEKYANFLASQVPPPSRLGDPAEYAHVQAILNPPLNG 248
Db 174 RNIVRYNIAAGMIESDMTALSLSPRIKEATLQIPM-KFEGQAEQVADLTVPFAGQDYLTG 232
QY 249 EYIRLDGAIIRM 259
Db 233 QVTAIDGGLSM 243

```

AAU37767	ID	AAU37767	standard; Protein; 243 AA.
XX	XX		
XX	AC	AAU37767;	
XX	DT		
XX	XX	14-FEB-2002	(first entry)
DE		Streptococcus pneumoniae	cellular proliferation protein #195.
XX	XX		
KW	XX	Antisense; prokaryotic	cellular proliferation protein;
XX	XX	antibiotic; antibacterial;	drug design.
OS		Streptococcus pneumoniae.	
XX	XX		
PN		WO200170955-A2.	
XX	XX		
PD		27-SEP-2001.	
XX			
PF		21-MAR-2001; 2001WO-US09180.	
XX	XX		
PR		21-MAR-2000; 2000US-191078P.	
PR		23-MAY-2000; 2000US-206848P.	
PR		26-MAY-2000; 2000US-207727P.	
PR		23-OCT-2000; 2000US-242578P.	
PR		27-NOV-2000; 2000US-253625P.	
PR		22-DEC-2000; 2000US-257931P.	
PR		16-FEB-2001; 2001US-269308P.	

New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -

CC The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the  
CC genes, their use in the discovery of novel antibiotics, the essential  
CC genes themselves and the encoded proteins. The prokaryotes used are  
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*  
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The  
CC invention is also useful for the identification of potential new targets  
CC for antibiotic development. The antisense nucleic acids can also be used  
CC to identify proteins used in proliferation, to express these proteins,  
CC and to obtain antibodies capable of binding to the expressed proteins.  
CC The proteins can be used to screen compounds in rational drug discovery  
CC programmes. The antisense nucleic acid sequence is also useful to screen  
CC for homologous nucleic acids which are required for cell proliferation in  
CC a wide variety of organisms. The present sequence represents an  
CC essential prokaryotic cellular proliferation protein.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

Query Match	25.4%;	Score 331.5;	DB 22;	Length 243;
Best Local Similarity	35.1%;	Pred. No. 2.5e-24;		
Matches	88;	Conservative 37;	Mismatches 103;	Indels 23;
				Gaps 6;

OY 15 ITGAGAGLGATTAERIVGGASAVLLDPNSGGE-----AAQKLGNNCYFAPADYTSE 68  
|||::|||:: ||::|| |::|  
Db 10 ITSSRGIGLAIHKFAAQGANITV----NSRGAISELLAEFBNYIKVYPISGDVSDF 65

Db 66 ADARKMIDQAIABELGSDVLYVNNAGI--TQDTLMKMK---TEADPEVKLVNLTGAFNM 119

QY 129 IRLVAGEMGQNEPDGGQGRGVIINTASVAAFEGVGQAAYSASKSGIVGMLTPIARDLAP 188

Db 120 TQSVL-----KPMKAREGAIINMSSVYGLMGNIGQANVAASKAGLIGFTKSVAREVAS 173

QY 189 IGRVMTIAPGLGFTPLTSLPEKVRNPLASQVPPFSRIGDPAEYAHVQAIIENPFNG 248

Db 174 RNRIRNVTAIPGMIIESDMTALISDKIKETLAQIPM-KEFGQAEQVADLTVFLAGODYLTG 232

QY 249 EVIRLDGALRM 259

Db 233 QVTAIDGGLSM 243

RESULT 11

AAU37988 standard; Protein; 243 AA.

AAU37988:

14-FEB-2002 (first entry)

Streptococcus pneumoniae cellular proliferation protein #417.

Antisense: prokaryotic cellular proliferation protein;

antibiotic; drug design.

Streptococcus pneumoniae.

WO200170955-A2.

27-SEP-2001.

21-MAR-2001; 2001WO-US09180.

21-MAR-2000; 2000US-191078P.

23-MAY-2000; 2000US-206848P.

26-MAY-2000; 2000US-207727P.

23-OCT-2000; 2000US-242578P.

27-NOV-2000; 2000US-253625P.

22-DEC-2000; 2000US-257931P.

16-FEB-2001; 2001US-269308P.

(ELITR) ELITRA PHARM INC.

Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

Yamamoto RT, Xu HH;

WPI: 2001-611495/70.

N-PSDB: AAS55847.

New polynucleotides for the identification and development of

antibiotics, comprise sequences of antisense nucleic acids -

Example 3; Seq ID No 13581; 511pp; English.

The invention relates to antisense inhibitors of genes essential to

prokaryotic cellular proliferation, their use in identifying the

genes, their use in the discovery of novel antibiotics, the essential

genes themselves and the encoded proteins. The prokaryotes used are

Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella

pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The

invention is also useful for the identification of potential new targets

for antibiotic development. The antisense nucleic acids can also be used

to identify proteins used in proliferation, to express these proteins,

and to obtain antibodies capable of binding to the expressed proteins.

The proteins can be used to screen compounds in rational drug discovery

programmes. The antisense nucleic acid sequence is also useful to screen

for homologous nucleic acids which are required for cell proliferation in

a wide variety of organisms. The present sequence represents an

essential prokaryotic cellular proliferation protein.

Notes: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

format directly from WIPO at

ftp.wipo.int/pub/published\_pot\_sequences.

Sequence 243 AA:

Query Match 25.4%; Score 331.5; DB 22; Length 243;

Best Local Similarity 35.1%; Pred. No. 2.5e-24;

Matches 88; Conservative 37; Mismatches 103; Indels 23; Caps 6;

QY 15 ITGASGIGLTAERLVQGSAYLIDLPSNGE-----AQARKKGNVCYAFADVTSE 68

Db 10 ITGSSRGIGLTAERLVQGSAYLIDLPSNGE-----AQARKKGNVCYAFADVTSE 65

QY 69 KDVCATLALAKGKFGGVAVANCAGIYASAKTYNLKKGQTHLDFORVLDVNMGTENV 128

Db 66 ADARKMIDQAIABELGSDVLYVNNAGI--TQDTLMKMK---TEADPEVKLVNLTGAFNM 119

QY 129 IRLVAGEMGQNEPDGGQGRGVIINTASVAAFEGVGQAAYSASKSGIVGMLTPIARDLAP 188

Db 120 TQSVL-----KPMKAREGAIINMSSVYGLMGNIGQANVAASKAGLIGFTKSVAREVAS 173

QY 189 IGRVMTIAPGLGFTPLTSLPEKVRNPLASQVPPFSRIGDPAEYAHVQAIIENPFNG 248

Db 174 RNRIRNVTAIPGMIIESDMTALISDKIKETLAQIPM-KEFGQAEQVADLTVFLAGODYLTG 232

QY 249 EVIRLDGALRM 259

Db 233 QVTAIDGGLSM 243

RESULT 12

AAU01032 standard; Protein; 243 AA.

AAU01032:

02-OCT-2001 (first entry)

CFE 35 protein sequence.

Antibacterial; vaccine; gene therapy; bacterial cell wall viability;

CFE; CEG; Conserved Essential Gene; Bacterial infection;

antisense therapy; antibiotic resistance.

Streptococcus pneumoniae.

WO200149721-A2.

12-JUL-2001.

29-DEC-2000; 2000WO-US35604.

30-DEC-1999; 99US-0174089.

(BRIM ) BRISTOL-MYERS SQUIBB CO.

Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Brucoleri RE;

Thamassil JA;

WPI: 2001-496721/54.

N-PSDB: AAH90731.

Nucleic acids encoding conserved essential genes involved in bacterial

replication which are potential targets for the treatment of antibiotic

resistant bacterial infections -

Claim 27; Page 273; 380pp; English.

The present invention relates to nucleic acids (AAH90701-AAH90918)

encoding polypeptides (AAU01002-AAU01144), which are essential for the

viability of a bacterial cell wall. The acronym CFE stands for "CEG For

Expression", where CEG stands for "Conserved Essential Gene". The nucleic





XX Hasselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;  
PI Yamamoto RT, Xu HH;  
XX  
DR WPI; 2001-611495/70.  
XX N-PSDB; AAS53187.

PT New polynucleotides for the identification and development of  
XX antibiotics, comprise sequences of antisense nucleic acids -  
XX

PS Example 3; Seq ID No 10921; 51pp; English.

XX The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the  
CC genes, their use in the discovery of novel antibiotics, the essential  
CC genes themselves and the encoded proteins. The prokaryotes used are  
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*  
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The  
CC invention is also useful for the identification of potential new targets  
CC for antibiotic development. The antisense nucleic acids can also be used  
CC to identify proteins used in proliferation, to express these proteins,  
CC and to obtain antibodies capable of binding to the expressed proteins.  
CC The proteins can be used to screen compounds in rational drug discovery  
CC programmes. The antisense nucleic acid sequence is also useful to screen  
CC for homologous nucleic acids which are required for cell proliferation in  
CC a wide variety of organisms. The present sequence represents an  
CC essential prokaryotic cellular proliferation protein.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pcl\_sequences.

XX Sequence 245 AA;

Query Match 24.8%; Score 323.5; DB 22; Length 245;  
Best Local Similarity 33.7%; Pred. No. 1.6e-23;  
Matches 84; Conservative 39; Mismatches 107; Indels 19; Gaps 5;

QY 15 ITGASGIGLTAERIVQGSATLLD---LPMSGEAOKKLGNNCPAPADVTEKD 70  
DB 10 ITGSTRGKGAVALAFKESANIVNGRSEETTPQROETL--RGVCICIGSGISPFDA 67  
QY 71 VQTALALAKGRFGRVAVNCAIYAVASKYTNLKKGGTHLEDFRVLVDVNLMTFNVIR 130  
DB 68 AGEMIAQATVDLGSIDILVNNAGIT-----NDKILLMTREDFENACIDIVLGTFFMTO 121  
QY 131 LVAGMGONEDDQGGORVITNTASVAFEGVQVQQAASAKSGIYGTLPIDALPIG 190  
DB 122 QAVKRMNQ-----RSGRIITMASVSGLMGNVQQAATAASKAGVGTKSVAKEVAPRG 175  
QY 191 IRVMTIAPGLTGTPLLTSLPEKRVNFTLASQVPEPRLDPPAEVHLVQALIENTPENGVEV 250  
DB 176 ITCNIAIAGFTQTEHTDVLSEKVTQNMNAQPLQGT-FQGVADVATAATFLAKSPYITGOV 234  
QY 251 IRLDGAIRM 259  
DB 235 VAVDGLVW 243

RESULT 15

AAU28344 standard; Protein; 257 AA.

AAU28344;

18-DEC-2001 (first entry)

Novel human secretory protein, Seq ID No 701.

Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;  
ischemia-reperfusion injury; haematopoiesis; cancer; neutrophil;  
transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
KW fertility; analgesic; pain; antigen.

OS Homo sapiens.

PN WO200166689-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US04942.

XX 07-MAR-2000; 2000US-0519705.

XX 19-MAY-2000; 2000US-0574454.

XX 17-JUN-2000; 2000US-0596193.

XX 14-JUL-2000; 2000US-0616847.

XX 19-SEP-2000; 2000US-0665363.

XX 20-OCT-2000; 2000US-0693267.

XX (HYSE-) HYSEQ INC.

XX Tang YI, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;  
PI Zhao QA, Yang Y, Dymnac RT, Zhang J, Chen R, Xue AJ, Wang J;  
XX

DR WPI; 2001-589934/66.  
XX N-PSDB; AAS45244.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries  
PT prepared from various human tissues, for diagnosis and treatment of  
XX cancer, neurological, inflammatory, and autoimmune disorders -  
XX

PS Example 2; SEQ ID No 701; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)  
CC and polynucleotides (II). (I) and (II) are useful for treating  
CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,  
CC ischemia-reperfusion injury, shock, sepsis, immune responses, and is  
CC involved in increasing haematopoiesis, stem cell survival, bone growth  
CC and remodeling. (I), (II) and modulators of (II) are useful for  
CC prophylaxis or treatment of one or more cancers. (II) is also useful for  
CC creating transgenic animals useful for studying the in vivo activities of  
CC the polypeptide as well as for studying modulators of the polypeptides.  
CC (I) induces the proliferation of neural cells and regeneration of nerve  
CC and brain tissue and is useful for the treatment of cerebral and  
CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,  
CC Parkinson's disease, Huntington's disease, and amyotrophic lateral  
CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic  
CC activity, regulation of haematopoiesis and is useful for treating myeloid  
CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
CC tissue growth, and in tissue repair, healing of burns, incisions,  
CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative  
CC disorders, for periodontal disease. Furthermore, (I) is also useful for  
CC gut protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissues, various immune deficiencies and  
CC disorders including severe combined immunodeficiency (SCID), bacterial or  
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,  
CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic  
CC reactions and conditions, such as asthma or other respiratory problems.  
CC In addition, (I) affects biorhythms or circadian cycles of rhythms,  
CC fertility, metabolism, catabolism, anabolism, storage or elimination of  
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides  
CC analgesic effects or other pain reducing effects, immunoglobulin like  
CC activity and can act as an antigen in a vaccine composition to raise an  
CC immune response. AAU28020-AAU28395 represent novel human secreted protein  
XX amino acid sequences of the invention.

XX Sequence 257 AA;

Query Match 24.3%; Score 317; DB 22; Length 257;  
Best Local Similarity 31.5%; Pred. No. 7.3e-23;



XX 02-APR-2001; 2001MO-US10720.  
PF 31-MAR-2000; 2000US-193920P.  
PR (MILL-) MILLENNIUM PHARM INC.  
PA Meyers RA, Rudolph-Owen LA;  
PI MPI; 2001-626438/72.  
DR N-PSDB; AAT0573.  
XX Novel isolated 21509 and 33770 polypeptides belonging to human  
PT dehydrogenase family members, useful for treating cancer, diabetes,  
PT atherosclerosis, glomerulonephritis, Crohn's disease, cirrhosis,  
PT multiple sclerosis -  
XX Claim 1(a); Fig 2; 140pp; English.

CC The present sequence is that of a novel human dehydrogenase,  
CC designated 21509. The protein has a significant number of  
CC structural characteristics in common with members of the  
CC dehydrogenase/oxidoreductase family. Its expression pattern  
CC suggests a role in tumour development. The invention provides  
CC 21509 and 33770 nucleic acids, antisense molecules, recombinant  
CC expression vectors, host cells and transgenic animals in which a  
CC 21509 or 3370 gene has been introduced or disrupted. It also  
CC provides 21509 and 33770 proteins, fusion proteins, antigenic  
CC peptides and antibodies, and methods for screening for compounds  
CC that modulate the expression or activity of 21509 or 33770  
CC polypeptides or nucleic acids. Such modulators are used in methods  
CC for inhibiting the proliferation or migration, or inducing the  
CC killing, of 21509- or 33770-expressing cells, especially the  
CC hyperproliferative and/or metastatic cells of a soft tissue tumour,  
CC solid tumour or metastatic lesion, especially ovarian cancer, colon  
CC cancer, lung cancer and liver cancer (claimed). Modulator  
CC compounds are also used in claimed methods of modulating fatty acid  
CC biosynthesis or retinoid biosynthesis in a cell. 21509 and 33770  
CC nucleic acids can also be used to prepare diagnostic probes and in  
CC gene (including antisense) therapy.

XX Sequence 237 AA;

Query Match 24.1%; Score 314; DB 22; Length 237;  
Best Local Similarity 32.0%; Pred. No. 1.3e-22;  
Matches 81; Conservative 41; Mismatches 105; Indels 26; Gaps 5;

QY 12 VAVITGASGIGLTAERLVGOGASAVILDPNSGGEAQAARKLNCCVPAPADYTSKDY 71  
DB 4 VCAIFGSGRGIGRVAQAQMARKGYRLAIARNLBGAAGAAGDGLDHLASCDVAKHDV 63  
QY 72 QTAALAGKFRGVDVAVNCAGI-----AVASKTYNLKGGQTHLEDFQRYLVNLTGTF 126  
DB 64 QNTPEEMKHLGRNFTLVNAGINRDSLVYRKT-----EDMVSGLHNLGSM 112  
QY 127 NVIRLVAGEGQNEPDGOGGVITINNTASVAAPFEGVQAAYASKSGIGVMTLPFARDL 186  
DB 113 LTCKAAMRAMIOQ-----OGGSIVNVOISIVGLKNSQSYASAKGGLVGFSPALKEV 166  
QY 187 APIGIRVMTIAPGLFETPLTSLPEKVRNPLASOVPPPSRLGDPAEVAHLVQATITENPFL 246  
DB 167 ARKATRVNVVAPGPFHTMDLKEE---HLKKNPL-GRGRTIIVAHNAVIFLLESTYI 222  
QY 247 NGEVIRLDGAIRM 259  
DB 223 TGHVLVVDGLOL 235

RESULT 18  
AAB96397  
ID AAB96397 standard; Protein; 241 AA.  
XX  
AC AAB96397;

XX 29-OCT-2001 (first entry)  
DE Putative P. abyssi dehydrogenase #8.  
XX Hyperthermophilic archaeon; hyperthermophilic protein.  
XX Pyrococcus abyssi.  
XX FR2792651-A1.  
XX 27-OCT-2000.  
XX 21-APR-1999; 99FR-0005034.  
XX 21-APR-1999; 99FR-0005034.  
XX 21-APR-1999; 99FR-0005034.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX (IFRE-) IFREMER INST FR RECH EXPL MER.  
XX Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte C;  
XX Querellou J, Weissenbach J, Saurin W, Heilig R;  
XX MPI; 2001-126236/14.

PT New nucleotide sequences isolated from Pyrococcus abyssi encode  
PT proteins useful in industry -  
XX Claim 7; Pages 1087-1088; 1657pp; French.

CC The present invention relates to the genomic sequence of Pyrococcus  
CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is  
CC a hyperthermophilic archaeon, which is isolated from deep-sea  
CC hydrothermal vents. The present invention have various potential industrial  
CC uses, since the proteins are stable at very high temperatures, some up to  
CC 110 degrees centigrade.  
CC Note: This patent is in the same patent family as WO200065062, which  
CC contains additional sequences as shown in AAB99132-AA999143,  
CC AAH75903-AAH75920 and AAG64636.

XX Sequence 241 AA;

Query Match 23.9%; Score 312.5; DB 22; Length 241;  
Best Local Similarity 34.1%; Pred. No. 1.9e-22;  
Matches 87; Conservative 47; Mismatches 92; Indels 29; Gaps 7;

QY 8 VNSIVAVITGASGIGLTAERLVGOGASAVILDPNSGGEAQAARKLNCCVPAPADYTSKDY 60  
DB 4 LSKQVALITGASGIGRVAQAQMARKGYRLAIARNLBGAAGAAGDGLDHLASCDVAKHDV 60  
QY 61 APADVTSEKDYQTAALAGKFRGVDVAVNCAGIAVAASKTYNLKGGQTHLEDFQRYLVNLTGTF 120  
DB 61 VKADVSNREVRVEMVKKVIDKFRIDILINNAGI--LGKT---KPLEVTDDEMVRVLSV 115  
QY 121 NMGTNVIRLVAGEGQNEPDGOGGVITINNTASVAAPFEGVQAAYASKSGIGVMTLPFARDL 180  
DB 116 NLNGAFTVQEVRIY-----KKGKIVNASTAGKDGCTGVGPHYASKGGIATLTF 166  
QY 181 PIARDLAPIGIRVMTIAPGLFETPLTSLPEKVRNPLASOVPPPSRLGDPAEVAHLVQATITENPFL 240  
DB 167 NLRHRLAP-NILVNAVAPGVDPTDMLSEKKE---MLKSLSTGDIARPSEVAHNAVIFL 221  
QY 241 IENPFLNGEYIRLDG 255  
DB 222 LENDHITGEVIVDVG 236

RESULT 19  
AAU28156  
ID AAU28156 standard; Protein; 237 AA.  
XX  
AC AAU28156;

XX 18-DEC-2001 (first entry)  
 XX Novel human secretory protein, Seq ID No 325.  
 DE  
 XX Human: secreted protein; arthritis; Crohn's disease; sepsis; shock;  
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
 KW fertility; analgesic; pain; antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200166689-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PF 05-MAR-2001; 2001WO-US04942.  
 XX  
 PR 07-MAR-2000; 2000US-0519705.  
 PR 19-MAY-2000; 2000US-0574454.  
 PR 17-JUN-2000; 2000US-0596193.  
 PR 14-JUL-2000; 2000US-0616847.  
 PR 19-SEP-2000; 2000US-0665363.  
 PR 20-OCT-2000; 2000US-0693267.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;  
 PI Zhao QA, Yang Y, Dzmanac RT, Zhang J, Chen R, Xue AV, Wang J;  
 XX  
 DR N-PSDB; AAS45056.  
 DR  
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries  
 PT prepared from various human tissues, for diagnosis and treatment of  
 PT cancer, neurological, inflammatory, and autoimmune disorders -  
 XX  
 PS Example 4; SEQ ID No 325; 107pp; English.

CC analgesic effects or other pain reducing effects, immunoglobulin like  
 CC activity and can act as an antigen in a vaccine composition to raise an  
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein  
 CC amino acid sequences of the invention.  
 XX  
 SQ Sequence 237 AA;  
 QY Query Match 23.9%; Score 312; DB 22; Length 237;  
 Best Local Similarity 31.6%; Pred. No. 2e-22;  
 Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;  
 QY 12 VAVITGASGLGATLTERLVGOGASAVLDPNSGGEAAKKLGNNCVAPADYTSERY 71  
 4 VCAVFGSSRGIGRAVAVQALNAKRGYRLAVIARNLEGAAGAAGDGGDHLAFSCDVAKEDV 63  
 QY 72 QTALALAKGKFGVDVAVNCAGI-----AVASKTYNLKKGQRTLEDFOFVLDVNLGTF 126  
 64 QNTPEEMEKHLGKYNFLVNAAGINRGGLVRTT-----EDMYSQHLTNLGS 112  
 QY 127 NVIRLVAGENGONEPDGGGQGVYINTASYAAFEQGVGQANASASKGIYGMTLPAROL 186  
 113 LTCKAAARTMIQO-----OGGSIVNVGSIYGLKGNSSGQSVSASKGLVGFSLAKKEY 166  
 QY 187 APTGIRYMTIAPGLFGPRLITSLPEKYRNFLASQVFPFSLGDPARYAHLVQAIIENPL 246  
 167 ARKRTIRNVVAPGPVHTDMTKDKEE---HLKKNIPL-GRFGETIVAHAVVFLLESPI 222  
 QY 247 NGEVIRLDGAI RM 259  
 DB 223 TGHVLVVDGGLQL 235  
 DB  
 RESULT 20  
 AAB19928  
 ID AAB19928 standard; Protein: 237 AA.  
 XX  
 AC AAB19928;  
 XX  
 DT 19-MAR-2001 (first entry)  
 XX  
 DE Human oxidoreductase OXRD-3.  
 XX  
 KW OXRD-3; human; oxidoreductase; dehydrogenase; cell proliferation;  
 KW neurological disease; smooth muscle disease; autoimmune disease;  
 KW inflammation; antiproliferative; neuroprotective;  
 KW immunosuppressive; antiinflammatory; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 66 /note= "O-phosphorylated"  
 FT Misc-difference 95 /note= "O-phosphorylated"  
 FT Misc-difference 114 /note= "O-phosphorylated"  
 FT Region 3..184 /note= "short-chain dehydrogenase signature"  
 FT  
 PN WO200071679-A2.  
 XX  
 PD 30-NOV-2000.  
 XX  
 PF 19-MAY-2000; 2000WO-US13879.  
 PR 20-MAY-1999; 99US-0135049.  
 PR 27-MAY-1999; 99US-0136740.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Yue H, Tang YT, Baughn MR, Lu DAM;  
 XX  
 DR WPI: 2001-025146/03



OS Listeria monocytogenes.

PN WO200177335-A2.

PD 18-OCT-2001.

PF 11-APR-2001; 2001WO-FR01118.

PR 11-APR-2000; 2000FR-0004629.

PA (INSP) INST PASTEUR.

PI Buchrieser C, Franquet L, Couve E, Rusniok C, Fajhl H, Dehoux P, Dussauguet O, Cheouanet F, Nedjari H, Glaser P, Kunst F, Cossart P, Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Dammann E, Hain T, Berche P, Chardot A, Durant L, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J, Rose M, Voss H;

PI Rose M, Voss H;

PT Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment and prevention of *Listeria* and related bacterial infections, and

PT related polypeptides

PS Claim 6: SEQ ID No 1597; 192pp; French.

XX The present invention relates to the genome sequence of *Listeria monocytogenes* EGD-e (see AB03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in *L. monocytogenes* and related organisms, and for studying genetic polymorphisms and other genes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of *L. monocytogenes* and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate *L. monocytogenes*-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccine compositions for the treatment or prevention of infections by *L. monocytogenes* and related organisms.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pcl\\_sequences](http://wipo.int/pub/published_pcl_sequences).

CC Sequence 247 AA;

XX Query Match 23.68; Score 308.5; DB 23; Length 247;

XX Best Local Similarity 32.08; Pred. No. 4,7e-22;

XX Matches 83; Conservative 46; Mismatches 102; Indels 33; Gaps 7;

XX 7 SVKGLAVITGASGLGLATLAEPLVSGASAVLDDPNSGGEAQA---KRL---GNNC 58

XX 2 TLGGKAVAVVGGSGIGRIDAINLAKGANIFF---NYNGSEPAEEETAKLVAEGVEV 57

XX 59 VFNPADVTSEKDVOTATLAKKRGFRVDVNCAGTAVASKTYNLKGGQHTLEDQRYL 118

XX 58 EAKKANVALAEDDAFAKQALIEFRGRDILVNNAGITRDLNLRKME-----DEMDVY 111

XX 119 DVNLMTGFNVLRLVAGMGONEPDGSGRVIINTASVAEFGQVGAASAKSGIVGM 178

XX 112 NINLKGFTLCTKAVSRFMKQ-----RAKKIIMASVGLIGNAGQANYVASKAGVIGL 165

XX 179 TLPIARLAPLGIKRVMTIAPGLGTPPLTSLPEKVRNFIASQVPEPRLGDPREYALVQ 238

XX 166 TKTLARLAPLGIKRVMTIAPGLGTPPLTSLPEKVRNFIASQVPEPRLGDPREYALVQ 221

XX 239 AII-----ENFNLGEVIRLDGARIM 259

XX 222 AVFLASDASKYITGRTLSVDGGMV 247

RESULT 23

AAU28296

ID AAU28296 standard; Protein; 288 AA.

AAU28296;

18-DEC-2001 (first entry)

Novel human secretory protein, Seq ID No 653.

Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.

Homo sapiens.

WO200166689-A2.

13-SEP-2001.

05-MAR-2001; 2001WO-US04942.

07-MAR-2000; 2000US-0519705.

19-MAY-2000; 2000US-0574454.

17-JUN-2000; 2000US-0596193.

14-JUL-2000; 2000US-0616847.

19-SEP-2000; 2000US-0663653.

20-OCT-2000; 2000US-0693267.

(HYSE-) HYSEQ INC.

WPI; 2001-589934/66.

N-PSDB; AAS45196.

Novel polypeptides and nucleic acids obtained from cDNA libraries

prepared from various human tissues, for diagnosis and treatment of

cancer, neurological, inflammatory, and autoimmune disorders

Example 2; SEQ ID No 653; 107pp; English.

The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and

disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention.

Sequence 288 AA:

Query Match 23.0%; Score 300.5; DB 22; Length 288;  
Best Local Similarity 29.9%; Pred. No. 3,6e-21;  
Matches 84; Conservative 44; Mismatches 110; Indels 43; Gaps 6;

1 MAAACRSVKGIVAVITGGASGLGIAETAEFLVGGASAVLLDPLNSGGEAAKKGNNCYF 60  
10 MATETP-YAGKVAVVITGGRGIGAGIYRAFYNSGARVYICDKDSGGRALGELPGGCI 68  
61 APADVTSEKDVQATLALAKGFEGRDVAVNACGIAVASKTYNLKGGOTHTLEDFORVLDV 120  
69 SFCVTOEDDVKILVSTIRFRGLDCVNNAGHPP-----QREETSAGHGFOLLEL 123  
121 NLKGTFFVIRLVAGEMONEPDGCGRGVITNTASVAEFEGOVGOAAVSASKGIYGM 180  
124 NLGTYITLTKALPYLKSO-----GVNINISLVGAGIQAQAVYVAITKAAVAMTK 176  
181 PIADLAPIGIRVMTIAPGLFPLTSLPEKYANFLASGVPP----- 224  
177 ALADESPYGVAVNCISPGNIMTLMEE-----LAALMPDPRAITREGMLAQGRSV 228  
225 -----SRLGDPAEY-AHLVCAIENPFLNGEVIRLDGAIRM 259  
229 QIQPLGRMGQPAVEGAANAVFLASDANCTGIXLIVTGAEI 269

RESULT 24  
AAV54421

ID AAV54421 standard; Protein: 244 AA.

AC AAV54421;

DT 06-APR-2000 (first entry)

DE Amino acid sequence of a beta-ketoacyl-ACP reductase enzyme.

KW Beta-ketoacyl-ACP reductase: Type II fatty acid synthetase;

KM stereoselectivity: 4-chloroacetoacetic acid ester;

KM (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;

KM beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase;

KM polybeta-hydroxy fatty acid biosynthesis; optically active;

4-haol-3-hydroxybutyric acid ester.

Escherichia coli.

EP955375-A2.

10-NOV-1999.

10-MAY-1999; 99EP-0109403.

08-MAY-1998; 98JP-0126507.

21-OCT-1998; 98JP-0300178.

05-APR-1999; 99JP-0098205.

(DAIL ) DAICEL CHEM IND LTD.

Yamamoto H;

WPI; 2000-118183/11.

DR N-PSDB; AA245746.

PT Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -

PS Claim 3; Page 16-17; 34pp; English.

The present sequence represents a beta-ketoacyl-ACP reductase protein of *Escherichia coli*. The beta-ketoacyl-ACP reductase enzyme constitutes a type II fatty acid synthetase. The enzyme has an extremely high reducing activity and stereoselectivity towards 4-chloroacetoacetic acid ester. The specification describes a method for producing a (S)-4-halo-3-hydroxybutyric acid ester. The method comprises asymmetrically reducing 4-halo-acetoacetic acid ester or its derivative with beta-ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase, or acetoacetyl-CoA reductase constituting the polybeta-hydroxy fatty acid biosynthesis system. The novel method is used to produce optically active 4-haol-3-hydroxybutyric acid ester, with a high purity.

Sequence 244 AA:

Query Match 22.8%; Score 297.5; DB 21; Length 244;  
Best Local Similarity 30.4%; Pred. No. 5,6e-21;  
Matches 77; Conservative 50; Mismatches 111; Indels 15; Gaps 4;

9 KGLVAVITGGASGLGIAETAEFLVGGASAVLLDPLNSGGEAAKKGNNCYFAPADVTSE 68  
4 EGKIALVTGASRGIGRAIETLAARGAVIGTATSENQAQISDYLGAHGKGLMLNVTDP 63  
69 KDVQATLALAKGFEGRDVAVNACGIAVASKTYNLKGGOTHTLEDFORVLDVNLKGTFFV 128  
64 ASIESVLEKIRAFEGVDLIVNAGITRNLMRKD-----EDMNDIIEINLSSVRL 117  
129 IRLVAGEMONEPDGCGRGVITNTASVAEFEGOVGOAAVSASKGIYGM 188  
118 SKAVRAMMKK-----RHGRITITIGSVYGTMGNGOANYAAKAGLIGFSKSLAREVAS 171  
189 IGRVMTIAPGLFPLTSLPEKYANFLASGVPPSRLGDPAEYAHLYVO--AITENPFL 246  
172 RGITVAVVADPGLFETMTALSDDOAGITLAQVP-AGRLGAGQELANNVAFASDPAEAYI 230  
247 NGEVIRLDGAIRM 259  
231 TGETLHVNGMYM 243

RESULT 25

AAU34533 standard; Protein: 244 AA.

ID AAU34533

AC AAU34533;

DT 14-FEB-2002 (first entry)

DE E. coli cellular proliferation protein #114.

KW Antisense; prokaryotic cellular proliferation protein;

KM antibiotic; antibacterial; drug design.

Escherichia coli.

WO200170955-A2.

27-SEP-2001.

21-MAR-2001; 2001MO-US09180.

21-MAR-2000; 2000US-191078P.

23-MAY-2000; 2000US-206848P.

26-MAY-2000; 2000US-207727P.

23-OCT-2000; 2000US-242578P.

27-NOV-2000; 2000US-253625P.

22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.  
XX  
XX (ELITRA) ELITRA PHARM INC.  
PA  
XX  
XX Hasebeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT,  
PI Yamamoto RT, Xu HH;  
XX WPI; 2001-611495/70.  
DR N-PSDB; AAS52392.  
XX  
XX  
XX New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids -  
XX  
XX  
PS Example 3; Seq ID No 10126; 51bp; English.  
XX  
XX The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the  
CC genes, their use in the discovery of novel antibiotics, the essential  
CC genes themselves and the encoded proteins. The prokaryotes used are  
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*  
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The  
CC invention is also useful for the identification of potential new targets  
CC for antibiotic development. The antisense nucleic acids can also be used  
CC to identify proteins used in proliferation, to express these proteins,  
CC and to obtain antibodies capable of binding to the expressed proteins.  
CC The proteins can be used to screen compounds in rational drug discovery  
CC programmes. The antisense nucleic acid sequence is also useful to screen  
CC for homologous nucleic acids which are required for cell proliferation in  
CC a wide variety of organisms. The present sequence represents an  
CC essential prokaryotic cellular proliferation protein.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 244 AA:  
SQ  
Query Match 22.8%; Score 297.5; DB: 22; Length 244;  
Best Local Similarity 30.4%; Pred. No. 5.6e-21;  
Matches 77; Conservative 50; Mismatches 111; Indels 15; Gaps 4;  
QY 9 KGLVAVITGGAGSLGATATERTVGAGASAVLLDLPNSGGEAQAQKLGNNCVFAPADVTSE 68  
DB 4 EGRKIALVTGASRGIGRAITAEITLAAGAVIGTATSENGAGAIISDYLGAANGKGLMNTDP 63  
QY 65 KDVOTRALALAKGKFRVDVAVNACGIAVASKTYNKKQHTLEDFOHVLVDVNLMTFFNV 128  
DB 64 ASIESVLEKIRAEFEVDILVNNAGITDNLIMRKD-----EEMNDIETNLSVFR 117  
QY 129 IRLVAGEMQNEPDGQGVITINTASVAFAFGQVGAAYASASKGIYGMTPADLAP 188  
DB 118 SKAVRAMMK-----HGRITIGSVYGMNGGQANVAAKAGLIGFSKLAREVAS 171  
QY 189 IGIRVYTTAPGLFGPLTSLPEKVRNLAQVPPPSRLGDPAEYAHVQ--ATLENPFL 246  
DB 172 RGIITVNVVAPGFIETDMTRALSDDRAGILAQVP-AGRLGGADEIANNVAFLASDEAYI 230  
QY 247 NGEVIRLDGAI RM 259  
DB 231 TGETLHVNGSMY 243

Search completed: June 23, 2003, 14:28:26  
Job time : 42.6667 secs



Thu Jun 26 06:55:09 2003

us-09-931-186-4.rspt

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:22:37 ; Search time 31.6667 Seconds  
(without alignments)  
1698.262 Million cell updates/sec

Title: US-09-931-186-4

Perfect score: 1304

Sequence: 1 MAALVRSYKGLVAVITGAS.....ENPLNGEVIKLDGAIKMP 261

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriophage:\*  
17: sp.archaeop:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1240.5	95.1	252	4	Q96HDS
2	1162	89.1	261	11	Q96HDS
3	1158	88.8	261	11	Q96HDS
4	993	76.2	196	4	Q8TCV9
5	750	57.5	258	5	Q19102
6	720	55.2	255	16	Q910T0
7	711	54.5	255	16	Q8YBS0
8	689.5	52.9	252	16	Q8XWEO
9	671.5	51.5	250	16	Q06544
10	670	51.4	255	16	Q92YSL
11	667	51.2	253	16	Q96HMD
12	652	50.0	255	2	Q9AHY1
13	642	49.2	257	16	Q8UFI2
14	607	46.5	126	11	Q9DCX5
15	603.5	46.3	264	5	Q8T2L7
16	595	45.6	260	16	Q9ABU6

17	386	29.6	443	2	Q935J3	Q935J3 myxococcus
18	373.5	28.6	246	16	Q8XHL1	Q8XHL1 clostridium
19	355.5	27.3	244	16	Q89YD6	Q89YD6 streptococ
20	355	26.9	252	16	Q9HW15	Q9HW15 pseudomonas
21	343.5	26.3	249	16	Q97DA6	Q97DA6 clostridium
22	337.5	25.9	247	16	Q8R9W0	Q8R9W0 thermococcus
23	336.5	25.8	297	3	Q42774	Q42774 neurospora
24	333.5	25.6	246	16	Q9KA03	Q9KA03 bacillus ha
25	333.5	25.6	251	16	Q8YVTO	Q8YVTO anabaena sp
26	332	25.5	246	16	Q8YVTO	Q8YVTO bacillus ha
27	326.5	25.0	248	2	Q9KJF1	Q9KJF1 thauera aro
28	325.5	25.0	243	16	Q9FBC3	Q9FBC3 streptococ
29	324.5	24.9	260	4	Q96KK9	Q96KK9 lactococcus
30	323.5	24.8	261	13	Q8UMU4	Q8UMU4 oryzias lat
31	323	24.8	271	10	Q94G09	Q94G09 cucumis sat
32	322	24.7	262	2	Q91G98	Q91G98 streptomyce
33	322	24.6	263	16	Q9KJF4	Q9KJF4 streptomyce
34	321	24.5	261	6	Q8WMN4	Q8WMN4 macaca mula
35	320	24.5	271	10	Q94G10	Q94G10 cucumis sat
36	317.5	24.3	246	2	Q9EX74	Q9EX74 rhodococcus
37	317	24.3	299	17	Q97UK6	Q97UK6 streptomyce
38	315.5	24.2	260	16	Q88068	Q88068 streptomyce
39	315	24.2	267	10	P93697	P93697 vicia unqui
40	314.5	24.1	259	16	Q8U616	Q8U616 agrobacteri
41	313.5	24.0	240	17	Q9UFS4	Q9UFS4 pyrococcus
42	313	24.0	258	2	Q9F8V0	Q9F8V0 streptomyce
43	312.5	24.0	296	16	Q9ABX6	Q9ABX6 caulobacter
44	312.5	24.0	237	2	Q93HC0	Q93HC0 streptomyce
45	312.5	24.0	237	4	Q8MTW8	Q8MTW8 homo sapien
46	312	23.9	249	2	Q9AJT2	Q9AJT2 thauera aro
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48	311	23.8	244	16	Q8YD94	Q8YD94 brucella me
49	309.5	23.7	253	16	Q8ZFT5	Q8ZFT5 yersinia pe
50	309	23.7	253	16	Q8U759	Q8U759 agrobacteri
51	309	23.5	256	16	Q8ZBQ6	Q8ZBQ6 yersinia pe
52	306	23.3	236	11	Q91VT4	Q91VT4 mus musculu
53	303.5	23.3	247	16	Q8Y690	Q8Y690 listeria mo
54	303	23.2	248	16	Q8Y690	Q8Y690 agrobacteri
55	302.5	23.2	249	2	Q8LBS5	Q8LBS5 geobacillus
56	302	23.2	263	2	Q9SSE7	Q9SSE7 streptomyce
57	302	23.2	273	2	Q9FS01	Q9FS01 streptomyce
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59	301.5	23.1	260	17	Q8U3B3	Q8U3B3 pyrococcus
60	301.5	23.1	247	2	Q9ZFP3	Q9ZFP3 bacillus me
61	301	23.0	296	5	Q9XX28	Q9XX28 caenorhabdi
62	300.5	23.0	250	2	Q96840	Q96840 xanthobacte
63	300	22.9	252	17	Q97U04	Q97U04 sulfolobus
64	298	22.8	254	16	Q92PP8	Q92PP8 rhizobium m
65	297.5	22.8	258	16	Q93339	Q93339 mycobacteri
66	296.5	22.7	258	2	Q8VM75	Q8VM75 rhizobium s
67	296.5	22.7	245	16	Q8YD01	Q8YD01 brucella me
68	296	22.7	315	10	Q94GM3	Q94GM3 brassica na
69	296	22.7	320	10	Q93X62	Q93X62 brassica na
70	296	22.6	320	16	Q9FRT1	Q9FRT1 streptomyce
71	295	22.6	328	10	Q93X67	Q93X67 brassica na
72	295	22.6	328	17	Q9HQ41	Q9HQ41 halobacteri
73	294	22.5	255	17	Q9H041	Q9H041 halobacteri
74	294	22.5	265	16	Q9S2E4	Q9S2E4 streptomyce
75	293.5	22.5	267	2	Q91BG2	Q91BG2 leifsonia a
76	291.5	22.4	254	10	Q949M2	Q949M2 brassica na
77	291.5	22.4	270	4	Q9BPK1	Q9BPK1 homo sapien
78	291.5	22.4	270	4	Q9BPK1	Q9BPK1 homo sapien
79	291	22.3	246	2	Q93HB3	Q93HB3 streptomyce
80	291	22.3	255	16	Q8RDC3	Q8RDC3 thermococcus
81	291	22.3	258	16	Q930L5	Q930L5 rhizobium m
82	290	22.2	272	16	Q8YHBO	Q8YHBO brucella me
83	289.5	22.2	405	16	Q98A50	Q98A50 rhizobium l
84	289	22.2	243	16	Q8RC25	Q8RC25 fuscobacteri
85	287.5	22.0	247	2	Q93QF0	Q93QF0 azotobacter
86	287.5	22.0	303	10	Q9SCU0	Q9SCU0 arabidopsis
87	287	22.0	317	10	Q93X68	Q93X68 brassica na
88	286.5	22.0	244	16	Q8X815	Q8X815 escherichia
89	286.5	22.0	245	16	Q8RDB9	Q8RDB9 thermococcus

## ALIGNMENTS

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90 286.5 22.0 246 2 Q9RB80
91 285.5 21.9 254 16 Q9RT26
92 285 21.9 255 16 Q9PCQ2
93 284.5 21.8 246 2 Q9F519
94 284.5 21.8 257 16 Q9WYD3
95 284 21.8 256 17 Q8RTU5
96 283.5 21.7 253 16 Q8CH41
97 283.5 21.7 272 16 Q9RGL1
98 283 21.7 252 16 Q92PP0
99 283 21.7 275 16 Q9K4H0
100 282.5 21.7 521 16 Q9A7A9

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Q9RB80 burkholderi
Q9RT26 deinococcus
Q9PCQ2 xylella fas
Q9F519 streptomyce
Q9WYD3 thermotoga
Q8RTU5 methanosarc
Q8CH41 lactococcus
Q9RGL1 staphylococ
Q92PP0 rhizobium m
Q9K4H0 streptomyce
Q9A7A9 caulobacter

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RESULT 1
Q96HD5 PRELIMINARY; PRT; 252 AA.

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AC 096HD5:
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Similar to hydroxyacyl-coenzyme A dehydrogenase, type II.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strassberg R.;
RU Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC EMBL: BC008708; AA08708.1; -.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 252 AA; 25984 MW; F36BB71070CE872D CRC64;

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Query Match 95.1%; Score 1240.5; DB 4; Length 252;
Best Local Similarity 96.2%; Pred. No. 4.4e-78;
Matches 251; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

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QY 1 MAAAVRSKGLVAVITGASGLGATAEKLVGGASAVLLDLPNSGGEAOKKLGNNVF 60
DB 1 MAAACRSVKGLVAVITGASGLGATAEKLVGGASAVLLDLPNSGGEAOKKLGNNVF 60
QY 61 APADVTSKDYQYALAKKFKGRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORVLDV 120
DB 61 APADVTSKDYQYALAKKFKGRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORVLDV 120
QY 121 NLKGTENVIRLVAGEMQNEPDGQGRVITNTASVAEFEGYQAAVSASKSGIVGNTL 180
DB 121 NLKGTENVIRLVAGEMQNEPDGQGRVITNTASVAEFEGYQAAVSASKSGIVGNTL 180
QY 181 PIADLAPIGIRVMTIAGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHLYQAI 240
DB 181 PIADLAPIGIRVMTIAGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 232 IENPFLNGEVIRLDGAIKMP 252

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RESULT 2
Q99N15 PRELIMINARY; PRT; 261 AA.
AC 099N15:
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

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DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Short chain L-3-hydroxyacyl-CoA dehydrogenase.
GN HSD17B10 OR SCHAD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21095701; Pubmed=11165016;
RA He X.Y., Merz G., Chu C.H., Lin D., Yang Y.Z., Mehta P., Schulz H.,
RA Yang S.Y.;
RT "Molecular cloning, modeling, and localization of rat type 10 17beta-
RT hydroxysteroid dehydrogenase."
RL Mol. Cell. Endocrinol. 171:89-98(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC EMBL: AF233685; AAK15008.1; -.
DR HSSP: 070351; 166W.
DR MGD: MGI:1333871; Hsd17b10.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 261 AA; 27273 MW; F37IED8A15CFEFAF CRC64;

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Query Match 89.1%; Score 1162; DB 11; Length 261;
Best Local Similarity 88.1%; Pred. No. 1.2e-72;
Matches 230; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

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QY 1 MAAAVRSKGLVAVITGASGLGATAEKLVGGASAVLLDLPNSGGEAOKKLGNNVF 60
DB 1 MAAACRSVKGLVAVITGASGLGATAEKLVGGASAVLLDLPNSGGEAOKKLGNNVF 60
QY 61 APADVTSKDYQYALAKKFKGRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORVLDV 120
DB 61 APADVTSKDYQYALAKKFKGRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORVLDV 120
QY 121 NLKGTENVIRLVAGEMQNEPDGQGRVITNTASVAEFEGYQAAVSASKSGIVGNTL 180
DB 121 NLKGTENVIRLVAGEMQNEPDGQGRVITNTASVAEFEGYQAAVSASKSGIVGNTL 180
QY 181 PIADLAPIGIRVMTIAGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHLYQAI 240
DB 181 PIADLAPIGIRVMTIAGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261

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RESULT 3
Q9CTT3 PRELIMINARY; PRT; 261 AA.
AC 09CTT3:
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hydroxyacyl-coenzyme A dehydrogenase, type II.
GN HSD17B10 OR HADH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawal J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Marcu Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,  
 RA Norokoshi P., Rang B., Schoenbach M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.",  
 RL Nature 409:685-690(2001).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 DR EMBL: AK013340; BAB28800.1; -  
 DR HSSP: O70351; IEGW.  
 DR MGD: MGI:133871; Hsdl7b10.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT.1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 261 AA; 27273 MW; F36CD19C7FCEFAF CRC64;

Query Match 88.8%; Score 1158; DB 11; Length 261;  
 Best Local Similarity 87.7%; Pred. No. 2.2e-72;  
 Matches 229; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MAAYSVKGIYAVTGGASGLIATRELVVGGASAVLDDPNSGGEAOKLGNVVF 60  
 DB 1 MAAYSVKGIYAVTGGASGLIATRELVVGGASAVLDDPNSGGEAOKLGNVVF 60  
 QY 61 APADVTSEKDVOTALALAKGKRGVAVNACGIAVASKTYNKKQTHLEDFORVLDV 120  
 DB 61 APADVTSEKDVOTALALAKGKRGVAVNACGIAVASKTYNKKQTHLEDFORVLDV 120  
 QY 121 NLMGTENVIRLVAGEGNEPDDGGRGVITNTASVAAPEGVGAASAGVGMVL 180  
 DB 121 NLMGTENVIRLVAGEGNEPDDGGRGVITNTASVAAPEGVGAASAGVGMVL 180  
 QY 181 PIARDLAPIGIRVVTIAPGLFATPLTSLPEKVCNFIASQVPPSRIDPARYAHLVQAI 240  
 DB 181 PIARDLAPIGIRVVTIAPGLFATPLTSLPEKVCNFIASQVPPSRIDPARYAHLVQAI 240  
 QY 241 IENPFLNGEYIRLDGAIKROP 261  
 DB 241 IENPFLNGEYIRLDGAIKROP 261

RESULT 4  
 O8RCV9 PRELIMINARY; PRT; 196 AA.  
 AC O8RCV9;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DE Endoplasmic reticulum-associated amyloid beta peptide-binding protein  
 DE (fragment).  
 GN EPAB.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Deininger M.H., Meyermann R., Schluesener H.J.;  
 RT "Expression, release and induction of endoplasmic reticulum-associated  
 RT amyloid beta-binding protein in brain disease.",  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY092415; BAB18189.1; -  
 FT NON\_TER 1  
 FT SEQUENCE 196 AA; 20581 MW; 2400DE14966BAA6A CRC64;  
 SQ  
 Query Match 76.2%; Score 993; DB 4; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-61;  
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AKKIGNCVAPADVTSEKDVOTALALAKGKRGVAVNACGIAVASKTYNKKQTHL 110  
 DB 1 AKKIGNCVAPADVTSEKDVOTALALAKGKRGVAVNACGIAVASKTYNKKQTHL 60  
 QY 111 LEDFORVLDVNTMGTFVIRLVAGEGNEPDDGGRGVITNTASVAAPEGVGAAS 170  
 DB 61 LEDFORVLDVNTMGTFVIRLVAGEGNEPDDGGRGVITNTASVAAPEGVGAAS 120  
 QY 171 SKGIVGMTPIARDLAPIGIRVVTIAPGLFATPLTSLPEKVCNFIASQVPPSRIDP 230  
 DB 121 SKGIVGMTPIARDLAPIGIRVVTIAPGLFATPLTSLPEKVCNFIASQVPPSRIDP 180  
 QY 231 AEVAHLVQAIENPFL 246  
 DB 181 AEVAHLVQAIENPFL 196

RESULT 5  
 Q19102 PRELIMINARY; PRT; 258 AA.  
 AC Q19102;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Probable 3-hydroxyacyl-CoA dehydrogenase F01G4.2 type II (EC 1.1.1.35)  
 DE (Type II HADH).  
 GN F01G4.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Harris B.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-CoA + NAD(+) = 3-OXOACYL-CoA +  
 CC NADH.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC FAMILY (SDR).  
 DR EMBL: Z68341; CA92764.1; -  
 DR HSSP: O70351; IEGW.  
 DR wormPep: F01G4.2; CE03127.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT.1.  
 KW Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.  
 FT NP\_BIND 11 36 NAD (BY SIMILARITY).  
 FT ACT\_SITE 165 165 BY SIMILARITY.  
 SQ SEQUENCE 258 AA; 27143 MW; 86BF2568EE6902B3 CRC64;

Query Match 57.5%; Score 750; DB 5; Length 258;  
 Best Local Similarity 59.9%; Pred. No. 2.9e-44;  
 Matches 154; Conservative 35; Mismatches 66; Indels 2; Gaps 1;

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QY 123 MGTEVITLVAGSEMGONPDGOGGVITINTASVAFAEGOVGAAYASAKSGIVGMTLPI 182
DB 120 LGTEVITLVAGVLAHGEHEKNDANGGVYINTASVAFAFGOTGOSAKSYASKAITGMTLPI 179
QY 183 ARDLAPIGIRVMTIAPGLGFTPLTSLPEKYCNFLASOPEPSSRLGDPAEYAHVQAIIIE 242
DB 180 ARDFAGDGIREFVMTIAPGLMDPPLTSLPEKYSFLAQIIPNPSRLGHPHEVGAIVQHIIE 239
QY 243 NFELNGEVRILDDAIRM 259
DB 240 NGYLVNGETIRFDGALRM 256

RESULT 6
Q910T0 PRELIMINARY: PRT: 255 AA.
ID 0910T0:
AC 0910T0:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Probable short-chain dehydrogenase.
GN PA2554.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RX MEDLINE-20437337; PubMed-10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Bindman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz L., Toleltino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.U., Coulter S.N., Folger K.R., Kas A., Lardis K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RT Nature 406:959-964(2000).
RL Mature 406:959-964(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC EMBL; AE004683; AAC05942.1; -.
CC HSP; O70351; IE3S.
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; 1.
CC Oxidoreductase; Complete proteome.
SQ SEQUENCE 255 AA; 26426 MW; EB8FF28712D2936D CRC64;

Query Match 55.2%; Score 720; DB 16; Length 255;
Best Local Similarity 57.5%; Pred. No. 3.4e-42;
Matches 145; Conservative 39; Mismatches 66; Indels 2; Gaps 1;

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RESULT 7
Q8YBS0 PRELIMINARY: PRT: 255 AA.
ID 08YBS0:
AC 08YBS0:
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE 3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100).
DE BME110816.
GN BME110816.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_taxid=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-16M / ATCC 23456 / B10TYPE 1;
RX MEDLINE-20020109; PubMed-11756688;
RA Delvecchio V.G., Kapattal V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson T., Bhattacharyya A., Lykdis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Betnal A., Mazur M., Golsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Teleson J.-J.,
RA Haselkorn R., Kyriides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009715; AAL54058.1; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 255 AA; 26263 MW; 5CF61D4B37F6B730 CRC64;

Query Match 54.5%; Score 711; DB 16; Length 255;
Best Local Similarity 57.1%; Pred. No. 1.4e-41;
Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

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OX NCBI\_TaxID=305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GM11000;  
 RA MEDLINE-21681879; PubMed-1182852;  
 RA Salanoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S.,  
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
 RA Chander M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,  
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,  
 RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,  
 RA Weissenbach J., Boucher C.A.; of the plant pathogen *Ralstonia solanacearum*.  
 RT Genome sequence of the plant pathogen *Ralstonia solanacearum*.  
 RL Nature 415:497-502(2002).  
 DR EMBL; AL646070; CAD16241.1;  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR OXidoreductase; Complete proteome.  
 KW SEQUENCE 252 AA; 25642 MW; D6EEFACDA99179DF CRC64;  
 SQ

Query Match 52.9%; Score 689.5; DB 16; Length 252;  
 Best Local Similarity 57.1%; Pred. No. 4,2e-40;  
 Matches 145; Conservative 33; Mismatches 71; Indels 5; Gaps 3;

OY 8 VAGIYAVITGGASGIGLTAERLVGOGASAVYLDLPNSGGEAOKKLGNCVFAPADYTS 67  
 DB 3 INDQYFIVTGGASGIGLTAERLVGOGASAVYLDLPNSGGEAOKKLGNCVFAPADYTS 60  
 OY 68 EKDVOTATLAKGKRGYDVAVNCAGIAVASKTYNLLKGGQHTLLEDFORVLDVNLGTFN 127  
 DB 61 EADGAAVQAAT-SIGALAGLVNCAGIAPASRT--VCKAGPHLDQFARVININLIGTFN 117  
 OY 128 VRLVAGEGMEPPGOGRGVITNTASVAEFGOGVGAASASGSGVGMTPARPLA 187  
 DB 118 MRLATATATANAPNAGSERGVITNTASVAEFGOGVGAASGSGVGMTPARPLA 177  
 OY 188 PGIRVMTIAPGLFTPLTSLPEKVCNPLASQVFPSPRLGDPAYAHLYQAIIENPFLN 247  
 DB 178 RGIRVMTIAPGLFTPLTSLPEKVCNPLASQVFPSPRLGDPAYAHLYQAIIENPFLN 237  
 OY 248 GEYIRLDGAIKMP 261  
 DB 238 GEYIRLDGAIKMP 251

RESULT 9  
 O06544 PRELIMINARY; PRT; 250 AA.  
 AC 006544;  
 DT 01-JUL-1997 (TREMblrel. 04, Created)  
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Oxidoreductase, short-chain dehydrogenase/reductase family.  
 GN RY1144 OR MTC165.11 OR M1117.  
 OS Mycobacterium tuberculosis  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RA Cole S.T., Broesch R., Parthill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock R., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,  
 RA Honesty T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sutcliffe J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RA "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."

RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CDC 1551 / OSHKOSH;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickley E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Emdolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z95584; CAB09032.1;  
 DR EMBL; A8006996; AAK45436.1;  
 DR HSP; O70351.1; 153.  
 DR TIGR; M1177;  
 DR TubercuList; Rv1144;  
 DR InterPro; IPR002198; ADH\_short.  
 DR InterPro; IPR00205; NAD\_binding.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR Hypothetical protein; Complete proteome.  
 KW SEQUENCE 250 AA; 25787 MW; 123A1005A12BD56 CRC64;  
 SQ

Query Match 51.5%; Score 671.5; DB 16; Length 250;  
 Best Local Similarity 60.1%; Pred. No. 7,2e-39;  
 Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;

OY 9 KGIVAVITGGASGIGLTAERLVGOGASAVYLDLPNSGGEAOKKLGNCVFAPADYTS 68  
 DB 4 KDAVAVITGGASGIGLTAERLVGOGASAVYLDLPNSGGEAOKKLGNCVFAPADYTS 60  
 OY 69 KDVOATATLAKGKRGYDVAVNCAGIAVASKTYNLLKGGQHTLLEDFORVLDVNLGTFN 128  
 DB 61 AAVSNALELA-DSGPAVAVVNCAGTGNATRV--LSRDGVEPLAFAEKIYDINLVGTFN 117  
 OY 129 IRLVAGEGMEPPGOGRGVITNTASVAEFGOGVGAASASGSGVGMTPARPLA 188  
 DB 118 IRLAERIAKTEP-IGERGVIINTASVAEFGOGVGAASASGSGVGMTPARPLA 176  
 OY 189 IGIRVMTIAPGLFTPLTSLPEKVCNPLASQVFPSPRLGDPAYAHLYQAIIENPFLN 248  
 DB 177 KLIRVMTIAPGLFTPLTSLPEKVCNPLASQVFPSPRLGDPAYAHLYQAIIENPFLN 236  
 OY 249 EYIRLDGAIKMP 261  
 DB 237 EYIRLDGAIKMP 249

RESULT 10  
 O092XSI PRELIMINARY; PRT; 255 AA.  
 AC 0092XSI;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Probable.  
 GN RA0792 OR SMA1452.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-1021;  
 RA Barnett M.O., Fisher R.F., Jones I., Komp C., Abola A.P.,  
 RA Bariloy-Hubler F., Bouzer L., Capela D., Gallibert F., Gouzy J.,  
 RA Gurjal M., Hong A., Hultzer L., Hyman R.W., Kahn D., Kahn M.D.,  
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,  
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;  
 RT "Nucleotide sequence and predicted functions of the entire

RT Sinochlozobium melliioti p5yMA.98aplasmi20.1.  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).  
 DR EMBL; AE007266; AAKc5450.1; "-  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PROSITE; PS00061; ADH\_SHORT; UNKNOWN\_1.  
 KW PfamId; Complete; P26529 MW; ED6C79/4203EDB67C CRC64;  
 QO SEQUENCE 235 AA; 26529 MW;

Query Match	51.4%;	Score 670;	DB 16;	Length 255;
Best Local Similarity	54.7%;	Pred. NO. 9.4e-39;		

QY 8 VKGLVAIVTGGASGSLGATAERLVQGAGASAVLLDLENSCGEAQAQKLNCCFEAPADVT 67  
 : | : ||| | : ||| | : ||| :  
 Db 3 LKSREFIWGCASSGIGAAVTRMLAQEGATVGLDLKPAGEEPPAELIGAAVFRNADVTN 62

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Oy      68 EKDYQTALLAKGKGRVDVAVMNCAGIAVASKTYNNKKQZHTLEDFQRLVDYNLMGTEN 127
        | | | | : | | | | | | | | | | : | | | | : | | | | |
Db      63 EADPTAALPAKQEEGHVHGILVNCAGTAPGEKI - LGRSGHALDSFAATVAVNLIGTEN 120

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QY      128 VIRLVAGEMQNEPQGGQKVIINTASVAFEGQVQQAASASKGSIIVGMLPIARDLA 187
      :||| | | ||| |:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      121 MIRLAEFVMSQGEPPADGERGVIYNTASTIAAFDQIGQMAAASKGVAAALTLPAARELA 180
```

Qy 188 PIGIVMTIAPGLEFGIPLLISLPKCYCNFLASQVPPPSRLGIPAEVAHLVQALITENPFLN 247  
 ||||:||||: ||: :||: |||| |||| ||||: ||||  
 Db 181 RFGIVVTTIAPGIEFTPMAGMQDVALAASVPEPPRLGPAEEVAALVKHICENTMVLN 240

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OY      248 GEVIRLDGAIKMP 261
        |||||:|
DB      241 GEVIRLDGAIKMP 254

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RESULT 11  
Q98HM4  
TD CQ8HM4  
PRELIMINARY.  
PRT: 253 AA

AC	Q98HM4;
DT	01-OCT-2001 (TrEMBLrel. 18, Created)
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II.  
GN MLR2803.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria: Proteobacteria: alpha subdivision: Rhizobiaceae group:

OC Phyllobacteriaceae; Mesornizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=MAFE530309;  
RX MEDLINE=21082930; PubMed=11214968;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishinaday, Kiyokawa C., Kohna M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.,  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

RI Mesonizodinium Iot.?,  
RL DNA Res. 7:331-338(2000).  
DR EMBL: AF003000; BAB49842.1; -,  
DR InterPro: IPR002198; ADH\_short.

DR INTERPTIO; IPR001092; HLH\_BASIC,  
DR PFAM; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.

DR PROSITE; PS00038; NEIL1A\_LOOF\_NEIL1A; UNKNOWN\_1.  
KM Complete proteome.  
SQ SEQUENCE 253 AA; 25814 MW; 8832D90EB9BD3D2A CRC64;

Query Match 21.2%, Score 0077, DB 10, Length 200,  
 Best Local Similarity 54.4%, Pred. No. 1.5e-38,  
 Matches 137, Conservative 37, Mismatches 74, Indels 4, Gaps 1

[illegible]

RESULT 12  
Q9AHY1  
ID Q9AHY1  
PRELIMINARY;  
PRT; 255 AA.

DT	01-JUN-2001	(TREMBlrel. 17, Created)
DT	01-JUN-2001	(TREMBlrel. 17, last sequence update)
DT	01-JUN-2001	(TREMBlrel. 21, last annotation update)

GN *Pseudomonas putida*,  
OC Bacteria; Proteobacteria; gamma sub-division; Pseudomonadaceae;  
FADB2X.

```

OX      NCBI_TaxID=303;
RN      [1]
RP      SEQUENCE FROM N.A.

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RX MEDLINE=21150437; PubMed=11251808;  
RA Olivera E.R., Carnicero D., García B., Mirambres B., Moreno M.A.,  
Cáceda L., DiRusso C.C., Naharro G., Luengo T.M.; Validation of malbarotic  
RA

RT and *n*-phenylkanonic acids in *Pseudomonas putida* U: genetic studies  
RT and biotechnological applications.":  
MOL. MICROBIOL. 39:863-874(2001)  
MOL. MICROBIOL. 39:863-874(2001)

CC (SDR) FAMILY.  
 DR EMBL: AF290950: AAK18170.1; -  
 DR HSPB: C70351: 1E3S  
 DR T16002108: new short

DR Pfam: PF00106; adh\_short; 1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; UNKNOWN\_1.  
DR PROSITE: PS00061; ADH\_SHORT; UNKNOWN\_1.

Query Match	50.0%	Score 652	DB 2	Length 255
Best Local Similarity	54.5%	Pred No 1	5e-37	
Seq	SEQUENCE	255 AA	26003 MW	56B658D2E906E73F CRC64

Matches	134	Conservative	40	Mismatches	70	Indels	2	Gaps	1
QY	14	VITGASGLGATTAERTLVGGASAVLLDLP	SGSGEAAKRLGNNGVFAPADVTSEKDVQT	73					

Db 9 IVSGAASGLGTAATQMLVEAGAKXMI.VDLNQAWEAKREKREIGDNARFAVADI.SDEOAAQA 68

OY 74 ALALAKGFGRADVAVNCAGTAVASKTYNNKKGGTTHLEDFORVLDVNMIMGTENTVIRLVA 133

Db 69 AADAAASAFGSLQGLNCAGIVGAERY - ISKQPHGLASLARKVINVNLVSSFNLLKLA 126  
 QY 134 GEMGQEPDQGGORGVIIINTASVAAREGQVQAAASASKGIVGMLPIARDLAPIGIRV 193

DB 127 AAMAECAADEGERGVYINTASIAADGQIGQAAATASKGAIASLILPAARELARKGIRV 186  
CY 194 MTIAPLFGTDLITSLPEKVCNFIASQVPPPSRLDPAEYVAHLVQAIIEENPLNGEVIRL 253

DB 187 MTIAPGIFEPDMAGNTEEVNASIAGVPPPRGPRPOEYAAALARIHTEENSMNGEVIRL 246  
 QY 254 DGAIRM 259  
 DB 247 DGAIRM 252

RESULT 13  
 Q8UF12 PRELIMINARY; PRT; 257 AA.  
 AC Q8UF12;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II.  
 GN Atrv1415 OR AGR\_C\_2613.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Secubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
 RA Raymond C., Rouse G., Senphimmachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,  
 RA Nester E.W.;  
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 C58.";  
 RL Science 294:2317-2323(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Houtrel K., Goldman B.S., Cao Y., Askenazi M., Halling C., Millan L.,  
 RA Flanagan C., Crowell C., Gunson J., Lomo C., Sear C., Strub G.,  
 RA Cielo C., Slater S.;  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 Agrobacterium tumefaciens C58.";  
 RL Science 294:2323-2328(2001).  
 DR EMBL: AE009102; AAL42421.1;  
 DR EMBL: AE008067; AAK87207.1;  
 KW Complete proteome.  
 SQ SEQUENCE 257 AA; 26622 MW; FF74A61FC4B2B5C CRC64;

Query Match 49.2%; Score 642; DB 16; Length 257;  
 Best Local Similarity 51.7%; Pred. No. 9e-37;  
 Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

QY 243 NPFLNGEVIRLDGAIRMOP 261  
 DB 238 NDYMGNEVIRLDGAIRMOP 256

RESULT 14  
 Q9DCX5 PRELIMINARY; PRT; 126 AA.  
 AC Q9DCX5;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Hydroxyacyl-coenzyme A dehydrogenase, type II.  
 GN HSD17B10 OR HADH2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirni L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Bozell D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guatincio S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima T., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyokawa K., Wang K.H., Welter C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:665-690(2001).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC EMBL: AK002368; BAB22046.1;  
 DR HSSP: O70351; 1E6W.  
 DR MGD: MGI:1333871; Hsd17b10.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 126 AA; 13265 MW; 78FFB6D41B9989D CRC64;

Query Match 46.5%; Score 607; DB 11; Length 126;  
 Best Local Similarity 95.2%; Pred. No. 9e-35;  
 Matches 120; Conservative 2; Mismatches 4; Indels 0; Gaps 0;







ID	Q99YD6	PRELIMINARY;	PRT	244 AA.
8	AVTITGMXXRXSAGRGAPRRPRRL	----	ARSALFDLNDGGAALVAGLADGKARFENYVNS	63
67	SEKDVQTLALAKKGFQGVAVNACAGINAVASTYVNLKKGQFTLEDPGRVLDVNLKMTF			126
64	DEAAVTAALIDDAHDFGLGVLNVAAMCAITLGRV--LGRKGPMLPLGFGIVMVLVGSF			121
127	NVIRLVAGEMCQNEPDGOGGQGVIIINTASVAAEFGVGQAAVSASXGIVGTLPIARDL			186
122	INAKKAARMQHNENEGTGEGRVITINTASIAAYEGQIGQAAYASXGIVSWTLPIAREL			181
187	APIGIRVMTIAPGLEGPRPLSLRPEKY			213
182	SREGIRVNTIAPGVWTPMDGMPEAY			208
8	AVTITGMXXRXSAGRGAPRRPRRL	----	ARSALFDLNDGGAALVAGLADGKARFENYVNS	63
67	SEKDVQTLALAKKGFQGVAVNACAGINAVASTYVNLKKGQFTLEDPGRVLDVNLKMTF			126
64	DEAAVTAALIDDAHDFGLGVLNVAAMCAITLGRV--LGRKGPMLPLGFGIVMVLVGSF			121
127	NVIRLVAGEMCQNEPDGOGGQGVIIINTASVAAEFGVGQAAVSASXGIVGTLPIARDL			186
122	INAKKAARMQHNENEGTGEGRVITINTASIAAYEGQIGQAAYASXGIVSWTLPIAREL			181
187	APIGIRVMTIAPGLEGPRPLSLRPEKY			213
182	SREGIRVNTIAPGVWTPMDGMPEAY			208

AC Q99YD6:2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 21, Last annotation update)  
DE Putative beta-ketoacyl-ACP reductase (EC 1.1.1.100).  
GN PABG OR SPY1749.  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
OC Streptococcaceae; Streptococcus.  
OX NCBI\_Taxid=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;  
RX MEDLINE=21192684; PubMed=11296296;  
RA Ferrauti J.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
RA Primeaux C., Seate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes";  
RT Proc Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY:  
CC EMBL: AE006603; AAK34493.1; -  
CC HSSP: P50162; IAB1.  
CC InterPro: IPR002198; ADH\_short.  
CC InterPro: IPR001092; HLH\_basic.  
CC Pfam: PF00106; adh\_short; 1.  
CC PRINTS: PR01608; BACINASTINC.  
CC PRINTS: PR00080; SDRFAMILY.  
CC PROSITE: PS00061; ADH\_SHORT; 1.  
CC PROSITE: PS00038; HELIX\_LOOP\_HELIX; UNKNOWN\_1.  
CC Oxidoreductase; Complete proteome.  
SQ SEQUENCE 244 AA; 26002 MW; 67ECE23870D40D65 CRC64;  
Query Match 27.3%; Score 355.5; DB 16; Length 244;  
Best Local Similarity 35.4%; Pred. No. 4.2e-17;  
Matches 92; Conservative 41; Mismatches 102; Indels 25; Gaps 5

QY 8 VKGLVAITGASGIGLTAERLYGQGSAYVLLDLPNSGGERQAQKL-----GNNCFV 60  
DB 3 IKGRNIFLTGIRGILMAHOFASLEANIYL-----NGRSKISBELVASFTDGVTVTF 57  
QY 61 APADYTSKRDVOTALAKKFGFRVDVAVNCAGIYASAKTYNLRKGGTHTLEDFORVDV 120  
DB 58 ISGVSEASEKRAKRWNEAIESIGSIDVLYNNAGT-----NDKMLKMTBEDFERVAKI 111  
QY 121 NIMGFTNTRILYAGMGONEDPDGQGRVITINTASVAFEGOVGOAASAKSGGIVGNTL 180  
DB 112 NLGTGFNNTQSTL-----KPKIRKQAQAIINWSSVGLTGTIGQANTAAASAGNIGFTK 165  
QY 181 PIARLARIIGIRVMTIAPLFGTPILTSLPERVCNFIASOVFPFRLGDPAEVAHLVQAI 240  
DB 166 SVAREVAARNICVNAIAPGFIESDVTGLPEKMQQILISQIPW-KRICKAQGVANHLASPL 224  
QY 241 IENPLNGEVTIRLDGAIIRMQ 260  
DB 225 VEQDYITGVYAIADGMTMQ 244

RESULT 20  
Q9HWM15  
ID Q9HWM15 PRELIMINARY; PRT; 252 AA.  
AC Q9HWM15:  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE Probable short-chain dehydrogenase.  
GN PA4389.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_Taxid=287;  
RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 15692 / PAOI;  
 RX MEDLINE-2043737; PubMed-10984043;  
 RA Hickey C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Stover C.K., Brinkman F.S.S., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardis K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reiter J., Satter M.H., Hancock R.E.W., Lory S., Olson M.V.,  
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAOI, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 (SDS) FAMILY  
 DR EMBL; AE004854; AAG07777.1; -  
 DR HSSP; P50163; 2AE1.  
 DR InterPro; IPR002198; ADH\_short.  
 DR InterPro; IPR001064; Crystal11n.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.  
 KW Oxidoreductase, Complete proteome  
 SQ SEQUENCE 252 AA; 26720 MW; F1F445AB82C2D8DE CRC64;  
 Query Match 27.2%; Score 355; DB 16; Length 252;  
 Best Local Similarity 35.1%; Pred. No. 4,7e-17;  
 Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;  
 QY 8 VKGLVAVITGASGLATAEERLVGQASAVLLDPN-----SGGEAQAKKLG 55  
 DB 3 LKDKVITITGGCGGLRANGELLAGKARLALVDLNRERLDVAVACRAAGDAA----- 58  
 QY 56 NNCVFAADVTESEKDYOTALALAKGKGRVDVAVNCAGIYAVASKYNNKKGQTH--TLED 113  
 DB 59 -YCVNVADEQVTHHVAQVASDFGALNGLVNNAGILRDLITIKYVDGLSKKSLAQ 113  
 QY 114 FORVLVNLMTGTFNVRIVLAGEMGQ--NEPDGQGRGVITNTASVAAFEQGVQAAVYAS 171  
 DB 114 WQSVIVDNLTVGLCTREVAAKKTELKNE-----GALVNISSISR-AGNGQANTSA 165  
 QY 172 KSGIVGMTPIADLPIGIRVMTIAPGLFGLPLTSLPEKYCNFLASQVPPSRIGDPA 231  
 DB 166 KAGVADTVYMAKELARGIRVAGVAFLETETEMTAGMKPELLEKVTAGIPL-KRMGRV 224  
 QY 232 EYAHLYQAITENPFLNGEVIRLDGAR 259  
 DB 225 EIAHSAVYIRENDYVYGRVLELDGGLRL 252  
 RESULT 21  
 Q97DA6 PRELIMINARY; PRT; 249 AA.  
 AC Q97DA6;  
 DT 01-OCT-2001 (TRENBLrel. 18, Created)  
 DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE 3-ketocacyl-acyl carrier protein reductase.  
 GN CAC3574.  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
 OC Clostridiales; Clostridiaceae; Clostridium.  
 OX NCBI\_TaxID=1488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE-21359325; PubMed-11465286;  
 RA Neelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
 RA Gidson R., Lee H.W., Dubois J., Qiu D., Hiti J., Wolf Y.T.,  
 RA Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.,  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium *Clostridium acetobutylicum*.";  
 RL J. Bacteriol. 183:4823-4838(2001).

DR EMBL; AE007854; AAK81497.1; -  
 DR InterPro; IPR002198; ADH\_short.  
 DR InterPro; IPR001092; HLH\_basic.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR PROSITE; PS00038; HELIX\_LOOP\_HELIX; UNKNOWN\_1.  
 KW Complete proteome.  
 SQ SEQUENCE 249 AA; 26247 MW; B13D7EDAC21A626A CRC64;  
 Query Match 26.3%; Score 343.5; DB 16; Length 249;  
 Best Local Similarity 33.2%; Pred. No. 2,9e-16;  
 Matches 86; Conservative 56; Mismatches 96; Indels 21; Gaps 6;  
 QY 8 VKGLVAVITGASGLATAEERLVGQASAVLLDPN-----AKKIGNNVFAP 62  
 DB 5 LSGVAVAVTGTAGRGALALAKLAEGANLV-VNYSSEAEOTKLIKELDELAKAVAK 63  
 QY 63 ADVTEKDYOTALALAKGKGRVDVAVNCAGIYAVASKYNNKKGQTHLEDQFQVLDVNL 122  
 DB 64 ADISKYDEAEITIKKALDEYGVLDLVNNAITGKDLNLRKE-----EDFQSVINVL 117  
 QY 123 MGTNVRIVLAGEMGQNEPDGQGRGVITNTASVAAFEQGVQAAVYASGSGIVMTLPI 182  
 DB 118 KGAFNCKIKHYSRVMLK-----KSGKITINISVIGLIGNAGOVNTAAAGIIGTKSV 171  
 QY 183 ARDLAPIGIRVMTIAPGLFGLPLTSLPEKYCNFLASQVPPSRIGDPAEYAHLYQAIT 242  
 DB 172 AKELASQITVNAVAFGLIKSDMTDALDKORRESIYAVPL-NKVGAEADVNLVFLAS 230  
 QY 243 --NPLNGEVIRLDGAR 259  
 DB 231 DLSSITGGVIVVDGGMV 249  
 RESULT 22  
 Q9R9W0 PRELIMINARY; PRT; 247 AA.  
 AC Q9R9W0;  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Dehydrogenases with different specificities (related to short-chain  
 DE alcohol dehydrogenases).  
 GN PABG3 OR TREN472.  
 OS Thermoaerobacter tengcongensis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
 OC Thermoaerobacteriales; Thermoaerobacteriaceae; Thermoaerobacter.  
 OX NCBI\_TaxID=119072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MBAT / JCM11007;  
 RX MEDLINE-21392816; PubMed-11997336;  
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
 RA Tan H., Chen R., Wang J., Yu J., Yang H.,  
 RT "A complete sequence of *T. tengcongensis* genome.";  
 RL Genome Res. 12:689-700(2002).  
 DR EMBL; AE013105; AAM24694.1; -  
 KW Complete proteome.  
 SQ SEQUENCE 247 AA; 26606 MW; 357D82B8C60E7947 CRC64;  
 Query Match 25.9%; Score 337.5; DB 16; Length 247;  
 Best Local Similarity 34.3%; Pred. No. 7,4e-16;  
 Matches 87; Conservative 48; Mismatches 100; Indels 19; Gaps 6;  
 QY 12 VAVITGASGLATAEERLVGQASAVLLDPN--SGGEA--QAKKIGNNVFAPADVTS 67  
 DB 7 VAFVTSGRSGIRALAVLADGFNIATYVKDKSABEVEEYKKGVDLAKCDVSK 66  
 QY 68 EKDYOTALALAKGKGRVDVAVNCAGIYAVASKYNNKKGQTHLEDQFQVLDVNLMTFN 127  
 DB 67 YHEVKAVERKYEERGSIDVVVNNAGITKDLILKMBE-----EMDQVIVDNLKGAFN 120

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QY 128 VRLVAGEGQNEPDGQGGVYINTASVAEFGVGAAYASAKSGIVGMLPIARDIA 187
DB 121 VIKFASKYMIKK-----RKGIINISSYVGMGNQANVAAKAGIIGLTKRSYAKELA 174
QY 188 PIGIRMTIAPGIFGPELLTSLPEKVCNPLASQVPPSRIGDPAEYAHVQ--AIENPF 245
DB 175 SRGITYNAVAPGFIETDMTNLTKEDIKEMLKSIPL-KRAGPEEVAEYVAFLASSADY 233

QY 246 LNGEVIRLDGAIRM 259
DB 234 ITGOVINVDGWMV 247

RESULT 23
Q42774 PRELIMINARY; PRT; 297 AA.
ID 042774;
AC 042774;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 3-oxoacyl-(acyl-carrier-protein)-reductase.
GN OAR-1 OR BZA19.180.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
ON NCBI_TaxID=5141;
RX [1]
RP SEQUENCE FROM N.A.
RA Burger F., Bros B., Weiss H.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Altm V., Hobeisel J., Brandt P., Fatmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhapt G.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL: AF042860; AAB99799.1; -.
DR EMBL: AL390092; CAB98248.1; -.
DR HSSP: O70351; IB6W.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PRO0080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
KW Oxidoreductase.
SQ
SEQUENCE 297 AA; 8DC08FEDF584196F CRC64;

Query Match 25.8%; Score 336.5; DB 3; Length 297;
Best Local Similarity 31.6%; Pred. No. 1.1e-15;
Matches 97; Conservative 40; Mismatches 103; Indels 67; Gaps 8;

QY 5 VRASKGVAVITGASGLATAERLVGQASAVLLDLPNS-----GGGA 49
DB 1 MRSLLKQALITGGSSIGLAIARLLYBGCSTYLLGRTSTIGRASQSLLSQPLHSPA 60
QY 50 QAKTIGNNCVAPADVTSEKDVOTAL-ALAKGFRGVAVNAGIAVAS--KTYNLKK 105
DB 61 QQPSDFKRVSYHPLNVAASSWEDLQSNKSGKGRVDILINCAGITORSPLMKT----- 115
QY 106 GQHTLEDPRVLDVNMGTFFNTRLVAGEGQNEP-----DOGG----- 145
DB 116 -----SIEVEGLDLDNLRGTVLCKEFGRAMLRRRPSQCHPRYKADGGAGEVMEGTEET 171
QY 146 -----QGVLIINTASVAEFGVGAAYASAKSGIVGMLPIARDIAPIG 190
DB 172 GKSGKQGVREGVQENGVIIINVASLLAQGVIGTSVYAAKAGVGLTSLAHEGRSG 231
QY 191 IRWMTIAPGLFGPIPLTSLPEKVCNPLASQVPPSRIGDPAEYAHVQAIENPFLNGEV 250

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DB 232 IRVNAVLPFGIETDMTTLKNP-----SILQGIPL-GRGCTTQEVADALFLIKNRYANNCV 287
QY 251 IRLDGA 257
DB 288 LNLDDGL 294

RESULT 24
Q9KA03 PRELIMINARY; PRT; 246 AA.
ID Q9KA03;
AC Q9KA03;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 3-oxoacyl-(acyl-carrier-protein) reductase (EC 1.1.1.100).
GN FABG OR BH2451.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacilliales;
OC Bacillaceae; Bacillus.
ON NCBI_TaxID=86665;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C-125 / JCM 9153;
RA MEDLINE-20512582; Pubmed-11058132;
RA Takami H., Nakasone K., Takaki Y., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL: AP001515; BAB06210.1; -.
DR HSSP: P19992; IHDC.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PRO0080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase; Complete proteome.
SQ
SEQUENCE 246 AA; 26126 MW; 852B95BDBDEB9E90 CRC64;

Query Match 25.6%; Score 333.5; DB 16; Length 246;
Best Local Similarity 34.2%; Pred. No. 1.4e-15;
Matches 90; Conservative 42; Mismatches 102; Indels 29; Gaps 7;

QY 8 VKGLVAVITGASGLATAERLVGQASAVLLDLPNSGGE-----AQAKTIGNNCV 59
DB 2 LOGKTAIVTGAISRGIGRATAMELARHGAVVV---NYAGNKEKAEKVVAEIKELGVBAI 57
QY 60 PAPADVTSEKDVOTALAKAGFRGVAVNAGIAVASKTYNLKKGQHTLEDPRVLD 119
DB 58 AIGADVASESVQAMVKETIDIFGAVDILVNNAGITRDLEPKME-----EDWDVID 111
QY 120 VNLMTGFNTRLVAGEGQNEPDGQGGVYINTASVAEFGVGAAYASAKSGIVGM 178
DB 112 TUKGVGFHCSKAVTSPMK-----QGRGIINISSYVGAIGNQANVAAKAGVIGL 164
QY 179 TLPPIARDIAPIGIRMTIAPGLFGPELLTSLPEKVCNPLASQVPPSRIGDPAEYAHVQ 238
DB 165 TLTIAELANRNITVNAVAPGFIETDMTGELEDVKAQMLGOIPL-ARLGOPEEYAKAVR 223
QY 239 AIEN--PFLNGEVIRLDGAIRM 259
DB 224 FLASDDASLYLTGQTIHVNGWMV 246

RESULT 25
Q8YVTO PRELIMINARY; PRT; 251 AA.
ID Q8YVTO;
AC Q8YVTO;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

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DE 01-JUN-2002 (TrEMBLrel. 21, last annotation update)  
DE 3-oxoacyl-[acyl-carrier protein] reductase.  
GN FABG OR ALR1894.  
OS Anabaena sp. (strain PCC 7120).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
OX NCBI\_TaxID=103690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21595285; PubMed=11759840;  
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
RA Kishida Y., Iritiguchi M., Ishikawa A., Kawashima K., Kimura T.,  
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,  
RA Yasuda M., Tabata S.;  
RT "Complete genomic sequence of the filamentous nitrogen-fixing  
cyanobacterium Anabaena sp. strain PCC 7120.";  
RL DNA Res. 8:205-213(2001).  
RI EMBL; AF003587; BAB73593.1; -;  
DR InterPro; IPR002198; ADH\_short.  
DR InterPro; IPR001092; HLH\_basic.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00064; ADH\_SHORT; 1.  
DR PROSITE; PS00038; HELIX\_LOOP\_HELIX; UNKNOWN\_1.  
SQ Complete proteome.  
SQ SEQUENCE 251 AA; 26218 MW; 57D0712F8E6B698 CRC64;

Query Match 25.6%; Score 333.5; DB 16; Length 251;  
Best Local Similarity 33.1%; Pred. No. 1.4e-15;  
Matches 91; Conservative 46; Mismatches 97; Indels 41; Gaps 7;

QY 1 MAAAVRSVRLVAVITGASGLGATAERLVGGASA-----VLLDLPNSGG 47  
DB 1 MAITSENLRGQVAVVVGASRGIGRAITALELANTGATVVVNVASSSTADEVVAETGAGG 60  
QY 48 EAQAKKLGNNCVFAPADVTSEKDVQATALAKGKFGRVDAVAVACAGIAVASKTYNLKQG 107  
DB 61 EAVALK-----ADVSGVEQVDNLINGAIDKFKRIDILVNNAGITRDITLLRKRP-- 109  
QY 108 THHIEDQRYLDVNMKGTENVIRLVAGSEKGNEDDGGORGVITINIASVAAPFGVGOAA 167  
DB 110 ---EDQAVIDINLGLVFLCTRAVSKMLKQ-----RSGRIINITSVAGQGNPQAN 159  
QY 168 YSASKGIVGMLPIARDLPIGIRVWTIAPGLFGTPLTSLPEKYCNFLASQVPPPSRL 227  
DB 160 YSAKAGVIGFTVAKELASRGITVAVAPGFIATDMTSNLKSE---GILGYIPL-GRY 215  
QY 228 GDPREYAHLYQALLENP---FLNGEVIRLDGAI RM 259  
DB 216 GQPEIAGWVFLAADPAAYITGQVFNVGDMVM 250

Search completed: June 23, 2003, 14:32:44  
Job time : 33.6667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:47 ; Search time 7.83333 Seconds

(without alignments)  
1381.956 Million cell updates/sec

Title: US-09-931-186-4

Perfect score: 1304  
Sequence: 1 MAAVRSVKGLAVITGAS.....ENPFLNGEYTRLDGAIKMP 261

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	99.6	261	1	HCD2_HUMAN
2	1196	91.7	261	1	HCD2_BOVIN
3	1166	88.7	260	1	HCD2_RAT
4	1137	87.2	261	1	HCD2_MOUSE
5	908	69.6	255	1	HCD2_DROME
6	383.5	29.4	247	1	YD50_MYCTU
7	341	26.2	246	1	FABG_THEMA
8	334	25.6	261	1	FABG_HUMAN
9	334	25.6	320	1	FABG_CUPLA
10	328.5	25.2	244	1	FABG_VIBCH
11	315.5	24.2	260	1	DHB8_MOUSE
12	313.5	24.0	247	1	FAG1_SYNY3
13	309.5	23.4	246	1	FABG_BACSU
14	305	23.4	261	1	YK02_MYCTU
15	301	23.1	255	1	YWFD_BACSU
16	300	23.0	255	1	2BHD_STREX
17	294.5	22.6	548	1	YAVI_RHISN
18	293	22.5	249	1	BAV1_EUBSP
19	291.5	22.4	244	1	FABG_VIBHA
20	290.5	22.3	248	1	FABG_AQUAE
21	289.5	22.2	244	1	FABG_ECOLI
22	288	22.1	263	1	UCPA_SALTY
23	287.5	22.0	246	1	PHBB_ALCEU
24	286	21.9	248	1	PHAB_AICIS
25	284.5	21.8	256	1	Y019_THEMA
26	283.5	21.7	244	1	FABG_SALTY
27	281.5	21.6	246	1	NODG_AZOB
28	280	21.5	259	1	CMTB_PSEPU
29	279.5	21.4	241	1	PHBB_ZOORA
30	279.5	21.4	248	1	FABG_CHLMT
31	277.5	21.3	289	1	YHDF_BACSU
32	277	21.2	250	1	LINC_PSEPA
33	276	21.2	249	1	BAV2_EUBSP

34	276	21.2	263	1	UCPA_ECOS7
35	276	21.2	263	1	UCPA_ECOLI
36	276	21.2	263	1	FABG_ARATH
37	275	21.1	246	1	PHBB_CHRVI
38	272	20.9	250	1	LINC_PSEPA
39	272	20.9	251	1	Y325_THEMA
40	270.5	20.7	240	1	FAG2_SYNY3
41	270.5	20.7	247	1	FABG_CHDTR
42	269.5	20.7	251	1	DHKB_STROM
43	268.5	20.6	262	1	DHGB_BACME
44	267.5	20.5	336	1	TS2_MAIZE
45	266.5	20.4	241	1	PHBB_RHIME
46	266.5	20.4	242	1	FABG_HAEIN
47	264	20.2	247	1	FABG_MYCTU
48	261	20.0	261	1	DHGA_BACME
49	259	19.9	258	1	DHGB_BACSU
50	259	19.9	261	1	DHG3_BACME
51	259	19.9	261	1	DHG3_BACME
52	258.5	19.8	238	1	Y0XD_BACSU
53	258	19.8	261	1	DHG2_BACME
54	257	19.7	256	1	BUDC_KLEPN
55	257	19.7	261	1	DHG4_BACME
56	256	19.6	261	1	DHG4_BACME
57	254.5	19.5	261	1	FABG_RICPR
58	254	19.5	261	1	DHG3_BACSU
59	251.5	19.3	267	1	SORD_KLEPN
60	250.5	19.2	266	1	PGDE_HUMAN
61	250.5	19.2	285	1	YHXC_BACSU
62	250	19.2	285	1	Y4MP_RHISN
63	246.5	18.9	261	1	ACT3_STRCO
64	245.5	18.8	253	1	3BHD_COMTE
65	245	18.8	255	1	YV06_PSEAE
66	245	18.8	256	1	GNO_GLIOX
67	244.5	18.8	245	1	NODG_RHIS3
68	244.5	18.8	262	1	YXBG_BACSU
69	243	18.6	270	1	DHMA_FLAS1
70	241.5	18.5	258	1	BDHA_RHIME
71	239	18.3	255	1	BDHA_ECOLI
72	238	18.3	247	1	FABG_PSEAE
73	237.5	18.2	261	1	FAGCW_ECOLI
74	237	18.2	248	1	FABG_CHLPA
75	237	18.2	255	1	FABG_MYCAV
76	235	17.6	257	1	YXIF_BACSU
77	228.5	17.6	245	1	NODG_RHIME
78	227.5	17.4	894	1	FOX2_NEOCR
79	227.5	17.4	258	1	BDHA_ALCEU
80	226.5	17.4	242	1	PHAB_PARDE
81	226.5	17.4	243	1	TEN1_DARST
82	224.5	17.2	249	1	DEK2_STRYN
83	224.5	17.2	256	1	DHSG_RHOSH
84	224	17.2	254	1	IDNO_ECOLI
85	223.5	17.1	241	1	BUDC_KLETE
86	222.5	17.1	256	1	MTDH_UREFA
87	222.5	17.1	900	1	FOX2_YEAST
88	221.5	17.0	285	1	GS39_BACSU
89	221	16.9	255	1	FABG_MYCSM
90	220.5	16.9	272	1	PH1534_MYCOC
91	218.5	16.8	259	1	DHKL_STRYN
92	217	16.6	248	1	SRUD_ECOLI
93	217	16.6	248	1	Y452_LISIN
94	216.5	16.6	254	1	KDUD_BACSU
95	215	16.5	253	1	KDUD_ECOLI
96	213	16.3	134	1	FABG_ACTGC
97	212.5	16.3	248	1	DHBB_CALTA
98	212	16.3	281	1	Y432_LISMO
99	212	16.3	281	1	BPHB_COMTE
100	211.5	16.2	278	1	YHXD_BACSU
					Y4VA_RHISN

ALIGNMENTS

RESULT 1

HC02\_HUMAN STANDARD: PRT: 261 AA.  
 ID HC02\_HUMAN  
 AC Q99714;  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DE 15-JUN-2002 (rel. 41, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
 DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein) (Short-chain type dehydrogenase/reductase XH98G2).  
 GN HADH2 OR ERAB OR XH98G2 OR SCHAD.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE=97478528; PubMed=9338779;  
 RA Yan S.D., Fu J., Soto C., Chen X., Zhu H., Al-Mohanna F., Collinson K., Zhu A., Stern E., Saido T., Tomiyama M., Ogawa S., Rohrer A., Stern D.;  
 RA "An intracellular protein that binds amyloid-beta peptide and mediates neurotoxicity in Alzheimer's disease."  
 RT Nature 389:689-695(1997).  
 RL Nature 389:689-695(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Zhuchenko O.P., Wehnert M., Bailey J., Sun Z.S., Lee C.C.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Miller A.P., Willard H.F.;  
 RL "Chromosomal basis of X chromosome inactivation: Identification of a multigene domain in Xp11.21-p11.22 that escapes X inactivation."  
 RT Proc. Natl. Acad. Sci. U.S.A. 95:8709-8714(1998).  
 RL [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE=98221216; PubMed=9553139;  
 RA He X.Y., Schulz H., Yang S.Y.;  
 RL "A human brain L-3-hydroxyacyl-coenzyme A dehydrogenase is identical to an amyloid beta-peptide-binding protein involved in Alzheimer's disease."  
 RT J. Biol. Chem. 273:10741-10746(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Lung;  
 RA Strausberg R.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: BINDS INTRACELLULAR AMYLOID-BETA. BY INTERACTING WITH AMYLOID-BETA, IT MAY CONTRIBUTE TO THE NEURONAL DYSFUNCTION ASSOCIATED WITH ALZHEIMER DISEASE.  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL TISSUES BUT IS OVEREXRESSED IN NEURONS AFFECTED IN AD.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U96132; AAC51812.1; -  
 CC EMBL: U73514; AAB69858.1; -  
 CC EMBL: AF069144; AAC39900.1; -  
 CC EMBL: AF065555; AAC15902.1; -  
 CC EMBL: AF037438; AAC16419.1; -  
 CC EMBL: AF037438; AAC16419.1; -

DR EMBL: BC000372; AAH00372.1; -  
 DR HSSP: O70351; 1E3S.  
 DR Genew: HGNC:4800; HADH2.  
 DR MIM: 300256; -  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PRO0080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 KM Oxidoreductase; NAD.  
 FT NP\_BIND 12 37 NAD (BY SIMILARITY).  
 FT ACT\_SITE 168 168 BY SIMILARITY.  
 SQ SEQUENCE 261 AA; 26923 MW; 9E74F242E3BEFE1 CRC64;  
 Query Match 99.6%; Score 1299; DB 1; Length 261;  
 Best Local Similarity 99.6%; Pred. No. 8.4e-94;  
 Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MAAVRSYKGLVAVITGASGLGATPRLVGGASAVILDLPSNGGEAQAQKLNCCVF 60  
 DB 1 MAACRSYKGLVAVITGASGLGATPRLVGGASAVILDLPSNGGEAQAQKLNCCVF 60  
 QY 61 APADYTSKDVQOTALAKKGFGRVDAVAVNCAGIAVASKTYNKKGQHTLDEPQVLDV 120  
 DB 61 APADYTSKDVQOTALAKKGFGRVDAVAVNCAGIAVASKTYNKKGQHTLDEPQVLDV 120  
 QY 121 NLMGFENVIRLVAGEMGNEPDGQGRVITINTASVAAFEGOVGAAYSAKSGIVGNTL 180  
 DB 121 NLMGFENVIRLVAGEMGNEPDGQGRVITINTASVAAFEGOVGAAYSAKSGIVGNTL 180  
 QY 181 PIARDLPIGIRVMTIABGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHVQAI 240  
 DB 181 PIARDLPIGIRVMTIABGLFTPLTSLPEKVCNFIASQVPPSRIGDPAEYAHVQAI 240  
 QY 241 IENPFLNGEVRILDSAIRMP 261  
 DB 241 IENPFLNGEVRILDSAIRMP 261  
 RESULT 2  
 ID HC02\_BOVIN STANDARD: PRT: 261 AA.  
 AC Q02691;  
 DT 15-JUL-1998 (rel. 36, Created)  
 DT 15-JUL-1998 (rel. 36, Last sequence update)  
 DT 16-OCT-2001 (rel. 40, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).  
 GN HADH2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE-Liver;  
 RX MEDLINE=97214648; PubMed=9061028;  
 RA Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.;  
 RT "Cloning and expression of cDNA for a newly identified isozyme of bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into mitochondria."  
 RL Biochim. Biophys. Acta 1350:317-324(1997).  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
 CC -----  
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DR EMBL; AB002156; BAA19510.1; -  
 DR HSRP; 070351; 166W;  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KM Oxidoreductase; NAD; Mitochondrion.  
 FT NP\_BIND 12 NAD (BY SIMILARITY).  
 FT ACT\_SITE 168 BY SIMILARITY.  
 SQ SEQUENCE 261 AA; 27140 MW; 8C7572B6A9A9780 CRC64;

Query Match 91.7%; Score 1196; DB 1; Length 261;  
 Best Local Similarity 91.6%; Pred. No. 8e-86;  
 Matches 229; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAARSVKGLAVITGGASGLTARIVGSGASAVLLDLPNSGGEAOKKLGNNVFE 60  
 DB 1 MAARSVKGLAVITGGASGLTARIVGSGASAVLLDLPNSDGETQAKKLGKSAF 60  
 QY 61 APADVTSEKDVOTALAKGKFRVDVAVNCAGIAVASKTYNLKKGTHTLEDFQRLDV 120  
 DB 61 APADVTSEKDVOTALAKGKFRVDVAVNCAGIAVASKTYNLKKGTHTLEDFQRLDV 120  
 QY 121 NMAGFNVRLVAGMGONEPDSGQGVITNTASVAFEGVGQAASASGKGIYGMTL 180  
 DB 121 NMAGFNVRLVAGMGONEPDSGQGVITNTASVAFEGVGQAASASGKGIYGMTL 180  
 QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFILASQVFPRLDPAEYAHLYQAI 240  
 DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFILASQVFPRLDPAEYAHLYQAI 240  
 QY 241 ENPFLNGEVIIRLDGAIRMOP 261  
 DB 241 ENPFLNGEVIIRLDGAIRMOP 261

## RESULT 3

HCD2\_RAT STANDARD; PRT; 260 AA.

ID HCD2\_RAT 070351; 090YD;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
 DE (Endoplasmic reticulum-associated amyloid beta-peptide binding  
 DE protein).  
 GN HADH2 OR ERAB.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OC NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Gunn-Moore F.J., Tavaire J.M.;  
 RT "Rattus norvegicus amyloid beta-peptide binding protein (ERAB) mRNA."  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RA Yang S.-Y., He X.-Y.;  
 RT "Molecular cloning and characterization of the cDNA of rat brain short  
 RT chain L-3-hydroxyacyl-CoA dehydrogenase."  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RC TISSUE=Brain;  
 RX MEDLINE=20481418; PubMed=11023795;  
 RA Powell A.J., Read J.A., Banfield M.J., Gunn-Moore F., Yan S.D.,  
 RA Lustbader J., Stern A.R., Stern D.M., Brady R.L.;

RT "Recognition of structurally diverse substrates by type II  
 RT 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding  
 RT alcohol dehydrogenase (ABAD).";  
 RL J. Mol. Biol. 303:311-327(2000).  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; AF049878; AAC05747.1; -  
 DR EMBL; AF069770; AAF14853.1; -  
 DR PDB; 1E3W; 25-MAY-01.  
 DR PDB; 1E3S; 25-MAY-01.  
 DR PDB; 1E6W; 25-MAY-01.  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KM Oxidoreductase; NAD; Acetylation; 3D-structure.  
 FT INCT\_MET 0  
 FT MOD\_RES 1 ACETYLATION (BY SIMILARITY).  
 FT NP\_BIND 11 NAD (BY SIMILARITY).  
 FT ACT\_SITE 167 BY SIMILARITY.  
 FT CONFLICT 4 V -> C (IN REF. 2).  
 SQ SEQUENCE 260 AA; 27114 MW; 30F7E723A95F9227 CRC64;

Query Match 88.7%; Score 1156; DB 1; Length 260;  
 Best Local Similarity 88.1%; Pred. No. 1e-82;  
 Matches 229; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 2 AAARSVKGLAVITGGASGLTARIVGSGASAVLLDLPNSGGEAOKKLGNNVFA 61  
 DB 1 AAARSVKGLAVITGGASGLTARIVGSGASAVLLDLPNSGEGTEAKKLGKGNIFA 60  
 QY 62 PADVTSEKDVOTALAKGKFRVDVAVNCAGIAVASKTYNLKKGTHTLEDFQRLDV 121  
 DB 62 PADVTSEKDVOTALAKGKFRVDVAVNCAGIAVASKTYNLKKGTHTLEDFQRLDV 120  
 QY 122 LMGTENVRLVAGMGONEPDSGQGVITNTASVAFEGVGQAASASGKGIYGMTL 181  
 DB 122 LMGTENVRLVAGMGONEPDSGQGVITNTASVAFEGVGQAASASGKGIYGMTL 180  
 QY 181 IARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFILASQVFPRLDPAEYAHLYQAI 241  
 DB 181 IARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFILASQVFPRLDPAEYAHLYQAI 240  
 QY 242 ENPFLNGEVIIRLDGAIRMOP 261  
 DB 242 ENPFLNGEVIIRLDGAIRMOP 260

## RESULT 4

HCD2\_MOUSE STANDARD; PRT; 261 AA.

ID HCD2\_MOUSE 008736;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)  
 DE (Endoplasmic reticulum-associated amyloid beta-peptide binding  
 DE protein).  
 GN HADH2 OR HSD17B10 OR ERAB.  
 OS Mus musculus (Mouse).;





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DR EMBL: AE003507; AAF48797.1; -.
DR HSSP: 070351; 1E3W.
DR Flybase: FBgn0021765; scu.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
KM Oxidoreductase; NAD; Mitochondrion.
FT NP_BIND 6 31 NAD (BY SIMILARITY).
FT ACT_SITE 162 162 BY SIMILARITY.
FT MUTAGEN 33 33 L->Q: LETHAL ALLELE.
FT MUTAGEN 120 120 F->I: LETHAL ALLELE.
SQ SEQUENCE 255 AA; 26905 MW; F58690643FA0FD03 CRC64;

Query Match 69.6%; Score 908; DB 1; Length 255;
Best Local Similarity 68.9%; Pred. No. 1.6e-63;
Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VKGLVAVITGASGLTAERLVGOGASAVLLDIPNSGGEQAQKKGNNCFAPADYTS 67
DB 2 IKNAVSLVVGASGLGRATAEKRLAAGASVILLADLPSSKGNVAKELGKVFFVVDYTS 61
QY 68 EKDVOTALAKGREGVAVNAGIAVASTYLNKKGQHTLEDFOKVLVDVNLMTGFN 127
DB 62 EKDVSAALQTAQDKFGRDLDTVNCAGTAVKTFENKVAHRLDFORVINTVGTFFN 121
QY 128 VTRLVGEMGONPDGOGRGVYINTASVAFAFEGOVGAASASGKIGVMTLPIDRLA 187
DB 122 VIRLSGLMAGNEPDGORGVIYNTASVAFAFDGQICGAAYASASAAVAGMTLPIDRLS 181
QY 188 PIGIRVMTIAPGLFTPLLTSLPEKYCNFLASQVPPPSRLGDPAEYAHVQAIIENPFLN 247
DB 182 TGIRICTIAPGLFNPMLALPEKVRFLAKSIPPPQLGEPSEYAHVQAIIENPFLN 241
QY 248 GEYIRIDGALRMOP 261
DB 242 GEYIRIDGALRMOP 255

RESULT 6
YD50.MYCTU STANDARD: PRT; 247 AA.
ID YD50.MYCTU
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase RV1350 (EC 1.-.-.-).
DE FABG2 OR RV1350 OR MT1393 OR MTCY02B10.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteriales;
OC Actinomycetales; Corynebacteriales; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID-1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37Rv;
RX MEDLINE-98295987; PubMed-9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekla E.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornby T., Jagels K., Krogh A., Moisan J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Emdolaeva M.D., Salzberg S.L.,

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RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORP-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC
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CC
CC EMBL: Z75555; CA99983.1; -.
CC HSSP: 070351; 1E3S.
CC TIGR: MT1393; -.
CC TubercuList: RV1350; -.
CC InterPro: IPR002198; ADH_short.
CC Pfam: PF00106; adh_short.1.
CC PRINTS: PR00080; SDRFAMILY.
CC PROSITE: PS00061; ADH_SHORT.1.
KM Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT NP_BIND 9 34 NAD (BY SIMILARITY).
FT ACT_SITE 155 155 BY SIMILARITY.
SQ SEQUENCE 247 AA; 25871 MW; 76CA07892E7BB73 CRC64;

Query Match 29.4%; Score 383.5; DB 1; Length 247;
Best Local Similarity 38.9%; Pred. No. 6.7e-23;
Matches 96; Conservative 43; Mismatches 91; Indels 17; Gaps 5;

QY 13 AVITGASGLTAERLVGOGASAVLLDIPNSGGEQAQKKGNN--CVFAPAVTSEKD 70
DB 10 AVITGAGGLGLAICQRFVAGARVYLDVLEATEVAAKLGGDDVALAVRCVYQADD 69
QY 71 VOTALAKKGRGVAVNAGIAVASTYLNKKGQHTLEDFOKVLVDVNLMTGFNVIR 130
DB 70 VDILIRTAVEREGIDVAVNNAAGITRDATM-----RTMEQCPDQVAVHLKGTWNGTR 123
QY 131 LVASGEMGNEPDGOGRGVYINTASVAFAFEGOVGAASASGKIGVMTLPIDRLAPIG 190
DB 124 LAAATMRER-----KRAIVNMSVSGKVGWGTNYSRAKAGIVGTRAAKAEHLHG 177
QY 191 IRVMTIAPGLFTPLLTSLPEKYCNFLASQVPPPSRLGDPAEYAHVQAIIENPFLNG 248
DB 178 IRVNAIAPGLIRSAATEMPORIMDKLAIEYPM--GRAGEPEVSAVAFVLAASLSYWTG 236
QY 249 EYIRIDG 255
DB 237 TVLDVTVG 243

RESULT 7
FABG.THEMA STANDARD: PRT; 246 AA.
ID FABG.THEMA
AC Q9X248;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR TM1724;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales;
OC Thermotogaceae; Thermotoga.
OX NCBI_TaxID-2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MS8 / DSM 3109;
RX MEDLINE-99287316; PubMed-10360571;

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RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
 RT genome sequence of *Thermotoga maritima*.";  
 RL Nature 393:323-329(1999).  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
 CC PATHWAY.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AE001811; MAD36790.1; -  
 DR HSSP: P50162; 1AEL.  
 DR TIGR: TM124; -  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.  
 FT NP\_BIND 10 34 NADP (BY SIMILARITY).  
 FT ACT\_SITE 154 154 BY SIMILARITY.  
 FT SEQUENCE 246 AA; 26401 MW; 8C08904D28099142 CRC64;  
 SQ  
 Query Match 26.2%; Score 341; DB 1; Length 246;  
 Best Local Similarity 33.7%; Pred. No. 1.3e-19;  
 Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;  
 QY 8 VKGLAVITGASGLGATLAEKLVGGASAVLLDLPNSGGEA---QAKKLGNNCVAPAD 64  
 Db 3 LEGVVCILITGASGIGKATLTLFAOGATVIADISKENDLSVKEAGELPGKVDYVYN 62  
 QY 65 VTSEKDVQTLALAKGFGVNDVAVNACIAVASKYTNLKKGTHTLEDFORVLDPNVLNG 124  
 Db 63 VTDRODKVEVERVVOYGRIDVLVNNAGITRDALLVRMKE-----EMDAVINVNLKG 116  
 QY 125 TFNVIRLVAGMGONEDDGGGQGVIIINTASVAFEQGVQQAIVSASKGIVMTLPAR 184  
 Db 117 VFNVTQWVAVYMKQ-----RNGSLVNSVSVGIGNPGQTVYASKSGVIGMTTWAK 170  
 QY 185 DLAPIGRTVITAPGLFTPLITSPEKVCNFIASQVPPFSKGDPAEVAHLV--QALIE 242  
 Db 171 ELAGRNIRVNAVAPGLETETMTEKLEPKARETALSRIPL-GRGKPEEVAOVILLFLASDE 229  
 QY 243 NPELNGEIVRLDGA 257  
 Db 230 SSYVTGGVIGIDGL 244  
 RESULT 8  
 DH88\_HUMAN STANDARD; PRT; 261 AA.  
 AC Q92506; O9UI01;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-  
 DE beta-hydroxysteroid dehydrogenase 8) (K6 protein) (K6-6).  
 GN HSD17B8 OR HHE6 OR RING2 OR FABG1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Tubby B.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RP [2]  
 RP SEQUENCE OF 3-261 FROM N.A.  
 RX MEDLINE=97001166; PubMed=8612499;  
 RA Ando A., Kikuchi Y.Y., Shigenari A., Kawata H., Okamoto N., Shina T.,  
 RA Chen L., Ikemura T., Ade K., Kimura M., Inoko H.;  
 RT "cDNA cloning of the human homologues of the mouse K64 and K66 genes  
 RT at the centromeric end of the human MHC region.";  
 RL Genomics 35:600-602(1996).  
 CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.  
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +  
 CC NAD(P)H.  
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.  
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE LIVER AND PANCREAS,  
 CC LOWER IN THE SKELETAL MUSCLE AND KIDNEY.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AL031228; CAC38444.1; -  
 DR EMBL: D82061; BA011529.1; -  
 DR HSSP: O70351; 1E6W.  
 DR GeneW: HGNC:3554; HSD17B8.  
 DR MIM: 601417; -  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 DR Steroid biosynthesis; Oxidoreductase; NAD; Multigene family.  
 KW NP\_BIND 15 39 NAD (BY SIMILARITY).  
 FT ACT\_SITE 169 169 E -> R (IN REF. 2).  
 FT CONFLICT 117 117 E -> P (IN REF. 2).  
 FT CONFLICT 193 193 R -> P (IN REF. 2).  
 FT CONFLICT 208 208 Q -> K (IN REF. 2).  
 FT CONFLICT 212 212 Q -> K (IN REF. 2).  
 FT SEQUENCE 261 AA; 26974 MW; 8BBB2D7131714D71 CRC64;  
 SQ  
 Query Match 25.6%; Score 334; DB 1; Length 261;  
 Best Local Similarity 31.0%; Pred. No. 4.9e-19;  
 Matches 85; Conservative 55; Mismatches 100; Indels 28; Gaps 8;  
 QY 1 MAAYVRS-VKGLAVITGASGLGATLAEKLVGGASAVLLDLPNSGGEAQAQKTL----- 54  
 Db 1 MASOLQNRRLRSALAVLTGASGIGRAVSRLRGEATVAACDLDRAAQETVRLRGGGS 60  
 QY 55 -----GNVCVFAPADVTSKDVQTFALALAKGFGK-VDVAVNACGIAVASKYTNLKRQ 107  
 Db 61 KEGPPRGNHAF-QADVSEARAARCLLEQVQACFSRPSVYVSCGIIODEFLHMSG-- 117  
 QY 108 THTLEDFORVLDPNVLNGITFNVIRLVAGMGONEDDGGGQGVIIINTASVAFEQGVQAA 167  
 Db 118 -----DDMDKVIIVNKGFTFLVYQAAQALVSN-----CGRGSIIINISIVGKGVNGQTN 168  
 QY 168 VSASKGIVGMLPLPARDLAPIGRTVITAPGLFTPLITSPEKVCNFIASQVPPFSRL 227  
 Db 169 YASKRAGVIGLQTLARELGRHGRICNSVLPFLFATPMQVPOVAVDKITMLPM-GHL 227  
 QY 228 GDPAEVAHLVQ--ATLENPELNGEIVRLDGAIRM 259  
 Db 228 GDPEDVADVAVFLASEDSGYIITGTSVETGGLEW 261

RESULT 9  
FABG\_CUPLA  
ID FABG\_CUPLA STANDARD: PRT: 320 AA.  
AC P28643:  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-DEC-1992 (Rel. 40, Last annotation update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor  
DE (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).  
GN CLKR27.  
OS Cuphea lanceolata.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Eurosid II; Myrtales; Lythaceae; Cuphea.  
OX NCBI\_Taxid=3930;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92293104; PubMed=1376402;  
RA Klein B., Pawlowski K., Hoerlcke-Grandpierre C., Scheil J.,  
RA Toepfer R.;  
RT Isolation and characterization of a cDNA from Cuphea lanceolata  
RT encoding a beta-ketoacyl-ACP reductase.";  
RL Mol. Gen. Genet. 233:122-128(1992).  
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
CC PATHWAY.  
CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC  
CC PLASTIDS.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X64566; CAA45866.1; -  
DR PIR: S19832; S19832.  
DR HSSP: P50162; 1AEL.  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short; 1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KM Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast;  
KM Transit peptide.  
FT TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).  
FT CHAIN 62 320 3-OXOACYL-[ACYL-CARRIER PROTEIN]  
FT REDUCTASE.  
FT NP\_BIND 82 106 NADP (BY SIMILARITY).  
FT ACT\_SITE 227 227 BY SIMILARITY.  
SQ SEQUENCE 320 AA; 33103 MW; 06BAF0522B2B8C87 CRC64;

Query Match 25.6%; Score 334; DB 1; Length 320;  
Best Local Similarity 32.7%; Pred. No. 6.2e-19;  
Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;

QY 2 AAATRSYKGLVAVITGASGLIATERTLVGOGASAVLLDLPNSGGEA-----QAKKLN 56  
DB 69 AGAGSVSPVIVITGASRGIGKAIKALSTL-GKAGCVLVAVYASSKREAEVSKREIDAFGG 127  
QY 57 NCYFAPADVTSEKDVQTALALAKGKGRVDVAVNCGIAVASTYLNKKGQTITLEDPR 116  
DB 128 QALTFSGADSKEDVEMKITAVDANGVTDLVNNAGITRDGLMKRKSQ-----WGE 181  
QY 117 VLDVNLGTFNIVIRLVAGENGQNEPDGQGRVYINTASVAEFGGVQAAVSASRGIV 176  
DB 182 VIDNLITGVFLCQAQAAKIMKK-----KKRIINIASVYGLVGNAGQANSAKAGVI 235

QY 177 GKTLPIDAPLAPICIRVYWTAPGLFGTPILTSPDKVKNFLASGVPPSRIGDAEAYHL 236  
DB 236 GFTRTVAEYASRNINNVAVAPGISSDMTSKLDDINKILLETIPL-GRYGPPEVAVGL 294  
QY 237 VOATIEPN-----FLNGEVIRIDGAIKM 259  
DB 295 VEPALNPASSYVIGVFTIDGKTM 320

RESULT 10  
FABG\_VIBCH  
ID FABG\_VIBCH STANDARD: PRT: 244 AA.  
AC Q9K0H7:  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-  
DE acyl carrier protein reductase).  
GN Fabg or VC2021.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
OX NCBI\_Taxid=666;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=El Tor N16961 / Serotype O1;  
RX MEDLINE=20406633; PubMed=10952301;  
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,  
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
RA Fraser C.M.;  
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
RT cholerae".  
RL Nature 406:477-483(2000).  
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS  
CC PATHWAY.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AE004276; AAF95169.1; ALT\_INIT.  
DR HSSP: P19992; IHDC.  
DR TIGR: VC2021; -  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short; 1.  
DR PRINTS: PR00080; SDRFAMILY.  
DR PROSITE: PS00061; ADH\_SHORT; 1.  
KM Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.  
KM NP\_BIND 10 34 NADP (BY SIMILARITY).  
FT ACT\_SITE 151 151 BY SIMILARITY.  
SQ SEQUENCE 244 AA; 25566 MW; 9FB2E827BD7C3CE CRC64;

Query Match 25.2%; Score 328.5; DB 1; Length 244;  
Best Local Similarity 32.0%; Pred. No. 1.2e-18;  
Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;

QY 7 SVKGLVAVITGASGLIATERTLVGOGASAVLLDLPNSGGEAQAQKIGNCCVAFADVT 66  
DB 2 NIEGRVAVITGASRGIGKAIKALSTLGAERGAKYIGATSESGAQAISDYLDGNGKGMALNVT 61  
QY 67 SKDVQDTALALAKGKGRVDVAVNCGIAVASTYLNKKGQTHLEDPQRLVDVNLGTF 126

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Db      62 NBSIEAVKATIDEGVDILVNNAGITRDNLKMKK-----EEMSDIETITISIF 115
QY      127 NYIRLVAGMGVNEPDGQGVINTASVAFEGOVGAASASAGIVGTLPARDL 186
Db      116 RLKAVLRLGMMK-----RGRITVSGSVGTMGAGANAAKAGVIGTKSMAREV 169
QY      187 APGIRVMTAPGLFCTPLTSLPEKVCNPLASQVPPSRCDPAEYAHVQAITENP-- 244
Db      170 ASRGVYVNTVAPGFIETDWTKALNDEORTATLQVDP-AGRLDDPREIASAV-AFLASPEA 227
QY      245 -FLNGEVIRLDGAIRM 259
Db      228 AYTGETLHVNGM 243

RESULT 11
DH88_MOUSE STANDARD: PRT: 260 AA.
AC PS0171: Q60959; Q60958; Q921W2;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-
DE beta-hydroxysteroid dehydrogenase 8) (Ke6 protein) (Ke-6).
GN HSD17B8 OR HKE6 OR H2-KE6.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93180832; PubMed=8441417;
RA Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;
RT "Downregulation of Ke 6, a novel gene encoded within the major
RT histocompatibility complex, in murine polycystic kidney disease.";
RL Mol. Cell. Biol. 13:1847-1853(1993).
RN [2]
RP ERRATUM.
RA Aziz N., Maxwell M.M., St Jacques B., Brenner B.M.;
RL Mol. Cell. Biol. 13:6614-6614(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=96027630; PubMed=7559658;
RA Maxwell M.M., Nearing J., Aziz N.;
RT "Ke 6 gene. Sequence and organization and aberrant regulation in
RT murine polycystic kidney disease.";
RL J. Biol. Chem. 270:25213-25219(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L.,
RA Hall J., Lasky S., Hood L.;
RT "Sequence of the mouse major histocompatibility locus class II
RT region."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +
CC NAD(P)H.
CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOTOPES: A SHORT FORM (SHOWN HERE) AND A
CC LONG FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: KIDNEY, LIVER AND MODERATELY IN SPLEEN, HEART
CC AND BRAIN.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U34072; AAC53573.1; -
CC CC EMBL: U34072; AAC53574.1; -
DR EMBL: AF100956; AAC69902.1; -
DR HSSP: 070351; 166W.
DR MGD: MGI:95911; H2-Ke6.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PROSITE: PS00061; ADH_SHORT; 1.
DR Steroid biosynthesis; Oxidoreductase; NAD; Multigene family;
KM Alternative splicing.
FT NP_BIND 13 38 NAD (BY SIMILARITY).
FT ACT_SITE 168 168 BY SIMILARITY.
FT VARSPIC 257 260 GLFW -> MRPSMGGGGNRTQVYMRK (IN LONG
FT ISOFORM).
FT CONFLICT 16 16 G -> GSGVPSQ (IN REF. 3).
FT CONFLICT 17 17 MISSING (IN REF. 1).
FT CONFLICT 230 230 E -> EG (IN REF. 1).
SQ SEQUENCE 260 AA; 26645 MW; 19C712FCD168B08 CRC64;

Query Match 24.2%; Score 315.5; DB 1; Length 260;
Best Local Similarity 31.0%; Pred. No. 1,36-17;
Matches 85; Conservative 55; Mismatches 105; Indels 29; Gaps 9;

QY 1 MAAVRSYKGLVAVITGGA-SGLGLATNRERLYVGGAANVLIDLPNSGGEAOKLGN--- 56
Db 1 MASQLR-LRSALAVLVGTGAGSGIGRAISVRLAAAGAAVAACDDLGAAQDVIRLLSPGS 59
QY 57 -----NCVFAPADVTSEKDVOTALAKGKFR-VDVAVNCAIYAVSKTYNLRKQ 107
Db 60 EDGARPKRHAF-QADVSGQPAARLLLEVGACSRPSPVYVSCAGITRDFLLHME-- 116
QY 108 THTLEDFOVLVDNLMGTFNIVRLVAGMGVNEPDGQGVINTASVAFEGOVQAA 167
Db 117 ----EDMDRVAVNKKGFVLTYQAAALVSS-----GGRSIIINISSIGKVNIGQTN 167
QY 168 YSASKGIVGMLTPIARDLPIGIRVMTAPGLFCTPLTSLPEKVCNPLASQVPPSR 227
Db 168 YASSAGVIGLTQNAARLGRNRSVLPGLFATIPQTMKPRKVDKVIAMPL-GHM 226
QY 228 GDPAEYAHVQ-AITENPFLNGEVIRLDGAIRM 259
Db 227 GDPEDVADVAVAFELASDESGYITGASVEVSGILFM 260

RESULT 12
PGL1_SYNY3 STANDARD: PRT: 247 AA.
ID PGL1_SYNY3
AC P73574;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-l-acyl-carrier protein reductase 1 (EC 1.1.1.100) (3-
DE ketoacyl-acyl carrier protein reductase 1).
GN FABL1 OR SLR086.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita W., Sasamoto S., Kimura I.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).

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Query	Match	Query Match	Score	DB 1	Length	260
Db	10	GLVAVITGAGSGLGATETAEFLVGGGASAVLLDLPLNSGGEGAOAKKIGNNCVAPADVSEK	69			
Qy	7	GRVALVSGAGAGMGASHVRANVAEGAKKVFEDIDDESKAVALAELADARVHLDYTOPA	66			
Qy	70	DVQATLALAKRGFRGVDAVAVNCAGIAVASKTYNNKKGGTFTLEDFQRYLVDVNLGTFENV	129			
Db	67	QMTAAVDAVTAFAFGGILHVLVNNAGI-----LNTGTTEDVATLTQMORTLDVNLGVFLGI	120			
Qy	130	RLVAGEMQNPDPDGGGQVGVITINMSVAVEGGOVQAAYSASKGIVMTPIRLDAP	189			
Db	121	RAVY-----KPKENAGKSGIINISIGLACTVACHGYTFRKVRRLTSTALDELPS	174			
Qy	190	GIRVATVAPGLFGLPTLTSLEPKVCNLTASOVPPPSRLG---DPAEVAHLV--QATIE	244			
Db	175	GIRVASHIPGIVKPKMTDMVPEDI-----FOTALGRAAPEVSNLVVYTLASDESS	225			
Qy	245	FLNGEVRIDLG	255			
Db	226	YSTGAEFYVDG	236			

RESULT 15  
 YWFD\_BACSU STANDARD; PRT; 255 AA.  
 ID YWFD\_BACSU  
 AC P39640;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical oxidoreductase ywfd (EC 1.-.-.-).  
 YWFD OR IPA-82D.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID:1423;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168;  
 RA MEDLINE-95020537; PubMed-7934828;  
 RA Glaser P., Kunst F., Arnold M., Coudart M.P., Gonzales W.,  
 RA Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,  
 RA Plescan E., Santanu M., Schneider E., Schweizer J., Vertes A.,  
 RA "Bacillus subtilis genome project: cloning and sequencing of the 97  
 RT kb region from 325 degrees to 333 degrees".  
 RT Mol. Microbiol. 10:371-384(1993).  
 RN (2)  
 RC SEQUENCE FROM N.A.  
 RC STRAIN-168;





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Db 61 APADVTSEKDVOTATLALAKGKGRVDVAVNCAGIAVASRTYTLKKGQTHLEDFQRVLDV 120
QY 121 NMGTFNVIRLVAGGKQNEPPOGGORGIITNTASVAAFEQVGAATASNGGIYGMTL 180
Db 121 NMGTFNVIRLVAGGKQNEPPOGGORGIITNTASVAAFEQVGAATASNGGIYGMTL 180
QY 181 PIARDLAPIGIRVMTIAPGLFCTPLTSLPERVCNFIASQVFPSPRLGDPAPAEYAHVQAI 240
Db 181 PIARDLAPIGIRVMTIAPGLFCTPLTSLPERVCNFIASQVFPSPRLGDPAPAEYAHVQAI 240
QY 241 IENPFLNGEYIRLDGAI RMQP 261
Db 241 IENPFLNGEYIRLDGAI RMQP 261

RESULT 6
US-09-931-186-2
Sequence 2, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAR, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELETTIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOMALTER, RICHARD E.
APPLICANT: TEMPCEZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/RAD2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214R
US-09-931-186-2

Query Match 98.7%; Score 1287; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 1,1e-108;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAAVSVKGLVAVITVGASGLIATAERLVGGASAVLLDLPNSGGEQAOKLGNVCVF 60
Db 1 MAAACRSVKGLVAVITVGASGLIATAERLVGGASAVLLDLPNSGGEQAOKLGNVCVF 60
QY 61 APADVTSEKDVOTATLALAKGKGRVDVAVNCAGIAVASRTYTLKKGQTHLEDFQRVLDV 120
Db 61 APADVTSEKDVOTATLALAKGKGRVDVAVNCAGIAVASRTYTLKKGQTHLEDFQRVLDV 120
QY 121 NMGTFNVIRLVAGGKQNEPPOGGORGIITNTASVAAFEQVGAATASNGGIYGMTL 180
Db 121 NMGTFNVIRLVAGGKQNEPPOGGORGIITNTASVAAFEQVGAATASNGGIYGMTL 180
QY 181 PIARDLAPIGIRVMTIAPGLFCTPLTSLPERVCNFIASQVFPSPRLGDPAPAEYAHVQAI 240
Db 181 PIARDLAPIGIRVMTIAPGLFCTPLTSLPERVCNFIASQVFPSPRLGDPAPAEYAHVQAI 240
QY 241 IENPFLNGEYIRLDGAI RMQP 261
Db 241 IENPFLNGEYIRLDGAI RMQP 261
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RESULT 7
US-09-984-245-245
Sequence 245, Application US/09984245
Patent No. US20020165374A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/09/984,245
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,281
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,350
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,135
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/050,937
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,099
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,095
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,096
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,355
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,351
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-245-245

Query Match 87.9%; Score 1146; DB 9; Length 227;
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Thu Jun 26 '06:55:08 2003

us-09-931-186-4.rapb

Page 5

[illegible]

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1      RESULT 8
2      US-09-966-262-245
3      ; Sequence 245, Application US/09966262
4      ; Publication No. US20030050461A1
5
6      GENERAL INFORMATION:
7
8      APPLICANT: Young et al.
9      TITLE OF INVENTION: 87 Human Secreted Proteins
10     FILE REFERENCE: P2004P1
11     CURRENT APPLICATION NUMBER: US/09/966,262
12     CURRENT FILING DATE: 2001-10-01
13     PRIOR APPLICATION NUMBER: US 09/154,707
14     PRIOR FILING DATE: 1998-03-17
15     PRIOR APPLICATION NUMBER: PCT/US98/05311
16     PRIOR FILING DATE: 1998-03-19
17     PRIOR APPLICATION NUMBER: US 60/041,277
18     PRIOR FILING DATE: 1997-03-21
19     PRIOR APPLICATION NUMBER: US 60/042,344
20     PRIOR FILING DATE: 1997-03-21
21     PRIOR APPLICATION NUMBER: US 60/041,276
22     PRIOR FILING DATE: 1997-03-21
23     PRIOR APPLICATION NUMBER: US 60/041,281
24     PRIOR FILING DATE: 1997-03-21
25     PRIOR APPLICATION NUMBER: US 60/048,094
26     PRIOR FILING DATE: 1997-05-30
27     PRIOR APPLICATION NUMBER: US 60/048,350
28     PRIOR FILING DATE: 1997-05-30
29     PRIOR APPLICATION NUMBER: US 60/048,188
30     PRIOR FILING DATE: 1997-05-30
31     PRIOR APPLICATION NUMBER: US 60/048,135
32     PRIOR FILING DATE: 1997-05-30
33     PRIOR APPLICATION NUMBER: US 60/050,937
34     PRIOR FILING DATE: 1997-05-30
35     PRIOR APPLICATION NUMBER: US 60/048,187
36     PRIOR FILING DATE: 1997-05-30
37     PRIOR APPLICATION NUMBER: US 60/048,099
38     PRIOR FILING DATE: 1997-05-30
39     PRIOR APPLICATION NUMBER: US 60/048,352
40     PRIOR FILING DATE: 1997-05-30
41     PRIOR APPLICATION NUMBER: US 60/048,186
42     PRIOR FILING DATE: 1997-05-30
43     PRIOR APPLICATION NUMBER: US 60/048,069
44     PRIOR FILING DATE: 1997-05-30
45     PRIOR APPLICATION NUMBER: US 60/048,095
46     PRIOR FILING DATE: 1997-05-30
47     PRIOR APPLICATION NUMBER: US 60/048,131
48     PRIOR FILING DATE: 1997-05-30
49     PRIOR APPLICATION NUMBER: US 60/048,096
50     PRIOR FILING DATE: 1997-05-30
51     PRIOR APPLICATION NUMBER: US 60/048,355
52     PRIOR FILING DATE: 1997-05-30
53     PRIOR APPLICATION NUMBER: US 60/048,160
54     PRIOR FILING DATE: 1997-05-30
55     PRIOR APPLICATION NUMBER: US 60/048,351

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? PRIOR FILING DATE: 1997-05-30
? PRIOR APPLICATION NUMBER: US 60/048,154
? PRIOR FILING DATE: 1997-05-30
? PRIOR APPLICATION NUMBER: US 60/054,804
? PRIOR FILING DATE: 1997-08-05
? PRIOR APPLICATION NUMBER: US 60/056,370
? PRIOR FILING DATE: 1997-08-19
? PRIOR APPLICATION NUMBER: US 60/060,862
? PRIOR FILING DATE: 1997-10-02
? NUMBER OF SEQ ID NOS: 343
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 245
? LENGTH: 227
? TYPE: prt
? ORGANISM: Homo sapiens
US-09-966-262-245

```

```

Query Match Similarity 87.9%; Score 1146; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 5, 1e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 35 ASAVLLDLPNSGGEAQRKLGNNCVFADPADYTSKDYOTATALAKGKGRVDYAVNCAGI 94
DB 1 ASAVLLDLPNSGGEAQRKLGNNCVFADPADYTSKDYOTATALAKGKGRVDYAVNCAGI 60
QY 95 AVASTYMLKKGGOTTLDLDFQVLDVNLNGTFNTRLVAAGENGKNEPDGGGQGVIIYNTA 154
DB 61 AVASTYMLKKGGOTTLDLDFQVLDVNLNGTFNTRLVAAGENGKNEPDGGGQGVIIYNTA 120
QY 155 SVAAFEGGVGAQAAYSASKGGIYGMTLPILARDLAPIGIRYMTIAPGLFGTPLLTSPEKYC 214
DB 121 SVAAFEGGVGAQAAYSASKGGIYGMTLPILARDLAPIGIRYMTIAPGLFGTPLLTSPEKYC 180
QY 215 NFLAAQVPPPSRLGDPAEYAHLYQAATIEPFLNGEYIRLDGAIKRP 261
DB 181 NFLAAQVPPPSRLGDPAEYAHLYQAATIEPFLNGEYIRLDGAIKRP 227

RESULT 9
US-09-983-966-245
/ Sequence 245, Application US/09983966
/ Publication No. US20030060619A1
/ GENERAL INFORMATION:
/ APPLICANT: Young et al.
/ TITLE OF INVENTION: 87 Human Secreted Proteins
/ FILE REFERENCE: P2004P1
/ CURRENT APPLICATION NUMBER: US/09/983,966
/ CURRENT FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: 09/154,707
/ PRIOR FILING DATE: 1998-09-17
/ PRIOR APPLICATION NUMBER: PCT/US96/05311
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: US 60/041,277
/ PRIOR FILING DATE: 1997-03-21
/ PRIOR APPLICATION NUMBER: US 60/042,344
/ PRIOR FILING DATE: 1997-03-21
/ PRIOR APPLICATION NUMBER: US 60/041,276
/ PRIOR FILING DATE: 1997-03-21
/ PRIOR APPLICATION NUMBER: US 60/041,281
/ PRIOR FILING DATE: 1997-03-21
/ PRIOR APPLICATION NUMBER: US 60/048,094
/ PRIOR FILING DATE: 1997-05-30
/ PRIOR APPLICATION NUMBER: US 60/048,350
/ PRIOR FILING DATE: 1997-05-30
/ PRIOR APPLICATION NUMBER: US 60/048,188
/ PRIOR FILING DATE: 1997-05-30
/ PRIOR APPLICATION NUMBER: US 60/048,135
/ PRIOR FILING DATE: 1997-05-30
/ PRIOR APPLICATION NUMBER: US 60/050,937
/ PRIOR FILING DATE: 1997-05-30
/ PRIOR APPLICATION NUMBER: US 60/048,187
/ PRIOR FILING DATE: 1997-05-30
/ PRIOR APPLICATION NUMBER: US 60/048,099

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PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/048,352  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/048,186  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/048,069  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/048,095  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/048,131  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/048,096  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/048,355  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/048,160  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/048,351  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/048,154  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/054,804  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: US 60/056,370  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: US 60/060,862  
PRIOR FILING DATE: 1997-10-02  
NUMBER OF SEQ ID NOS: 343  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 245  
LENGTH: 227  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-983-966-245

Query Match  
Best Local Similarity 100.0%; Score 1146; DB 9; Length 227;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ASAVLLDLPNSGGEQAQKLGNNCFAPADVTSEKDVOTATLALAKGKRGVAVNACGI 94  
DB 1 ASAVLLDLPNSGGEQAQKLGNNCFAPADVTSEKDVOTATLALAKGKRGVAVNACGI 60  
QY 95 AVASKTYNLKKGGQTHTLEDFQFVLDVNLMTGFENVIRLVAGMGONEDDGGORGVIIINTA 154  
DB 61 AVASKTYNLKKGGQTHTLEDFQFVLDVNLMTGFENVIRLVAGMGONEDDGGORGVIIINTA 120  
QY 155 SVAAFEGVGOAAYASASKGIVGMLPLIARDLAPIGIRVMTIAPGLFTPLTSLPERVC 214  
DB 121 SVAAFEGVGOAAYASASKGIVGMLPLIARDLAPIGIRVMTIAPGLFTPLTSLPERVC 180  
QY 215 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMQP 261  
DB 181 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMQP 227

RESULT 10  
US-10-143-090-245  
Sequence 245, Application US/10143090  
Publication No. US20030069406A1  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 87 Human Secreted Proteins  
FILE REFERENCE: P2004P1  
CURRENT APPLICATION NUMBER: US/10/143,090  
CURRENT FILING DATE: 2002-05-13  
PRIOR APPLICATION NUMBER: 09/154,707  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 343  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 245  
LENGTH: 227  
TYPE: PRT

ORGANISM: Homo sapiens  
US-10-143-090-245

Query Match  
Best Local Similarity 100.0%; Score 1146; DB 9; Length 227;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ASAVLLDLPNSGGEQAQKLGNNCFAPADVTSEKDVOTATLALAKGKRGVAVNACGI 94  
DB 1 ASAVLLDLPNSGGEQAQKLGNNCFAPADVTSEKDVOTATLALAKGKRGVAVNACGI 60  
QY 95 AVASKTYNLKKGGQTHTLEDFQFVLDVNLMTGFENVIRLVAGMGONEDDGGORGVIIINTA 154  
DB 61 AVASKTYNLKKGGQTHTLEDFQFVLDVNLMTGFENVIRLVAGMGONEDDGGORGVIIINTA 120  
QY 155 SVAAFEGVGOAAYASASKGIVGMLPLIARDLAPIGIRVMTIAPGLFTPLTSLPERVC 214  
DB 121 SVAAFEGVGOAAYASASKGIVGMLPLIARDLAPIGIRVMTIAPGLFTPLTSLPERVC 180  
QY 215 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMQP 261  
DB 181 NFLASQVPPPSRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMQP 227

RESULT 11

US-09-920-923-41  
Sequence 41, Application US/09920923  
Publication No. US20030022273A1  
GENERAL INFORMATION:

APPLICANT: Pasamontes, Luis  
APPLICANT: Isyankov, Yuri  
TITLE OF INVENTION: Improved Fermentative Carotenoid Production  
FILE REFERENCE: Improved Fermentative Carotenoid  
CURRENT APPLICATION NUMBER: US/09/920,923  
CURRENT FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: 08/980,832  
PRIOR FILING DATE: 1997-12-01  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 388  
TYPE: PRT  
ORGANISM: Flavobacterium sp. R1534  
US-09-920-923-41

Query Match  
Best Local Similarity 51.0%; Score 664.5; DB 9; Length 388;  
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITGGASGLATAEKLVGOGASAVLLDLPNSGGEQAQKLGNNCFAPADVT 67  
DB 143 IEGRVTVVVGASGLGASASRMIAOGGAKVYIADL-----AEPKDAPEGVHAACDVID 196  
QY 68 EKDVOTATLALAKGKRGVAVNACGIASASTYNLKKGGQTHTLEDFQFVLDVNLMTGF 127  
DB 197 ATAQTATLALATDRFGRDLGIVNCAGIAPAEKRV--LGRGPGIGLDSFARAVYINLIGSP 254  
QY 128 VIRLVAGMGONEDDGGORGVIIINTASVAAFEGVGOAAYASASKGIVGMLPLIARDL 187  
DB 255 MARLAAPAMAKRNEPVR-GERGVIVNTASTAIODGOIGOVAYIASKRAQVAGALPMAKRD 313  
QY 188 PIGIRVMTIAPGLFTPLTSLPERVCNFLASQVPPPSRLGDPAEYAHVQAIIENPFLN 247  
DB 314 RHGIRVMTIAPGIFRPMLEGLPODVODSLGAAVPPPSRLGEPSEYEAALLHHIIPMLN 373  
QY 248 GEYIRLDGAIKMQP 261  
DB 374 GEYIRLDGAIKMQP 387

RESULT 12  
US-09-931-186-17  
Sequence 17, Application US/09931186

```
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELVIN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REUTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 17
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
US-09-931-186-17

Query Match
Best Local Similarity 31.2%; Pred. No. 2.3e-22;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;

QY 8 VGLVAVITGASGLATARLVGQASAVLLDLPNSGGEAQAARL-----GN 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 7 LLSALALVTGAGSGIGRAVSVRLAGEGATVACDDIDRAAAGETVLLGGPSKEGPPGN 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 NCVFAPADYTSERKQDTALAKKRGFR-VDAVAVACAGIAVASKTYNLKKGTHLEDFQ 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 67 HAAF-QADVSEARAACLEVOQACEPRPSVYVSCAGITODEFILLHSE-----DWD 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 RYLVNLMGTFNVIRLVAGEMGNPDGGRGVITINTASVAAPFEGVOGAAYSASKGI 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 120 KVIAYVILKGTFLVTAQAQALVSN-----GCRGSIINISSIVGKYGNGQIVYASKAGV 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 VGMTLPARDLAPFGRVNTIAPGLGFTPLTSLPEKYNCFLASQVPPFSRLDPAFYAH 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 175 IGLTQTARELGHGIRCNVSLPLGFLAPMTQKVPQKVDKITEMIPM-GRIGDPEVDAD 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 LVQ--AIENPFLNGEVIRLDGAIRM 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 234 VVAFLASEDSGYITGIVEVTGLFW 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-09-815-242-13360
Sequence 13360, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlson, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 13360
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-815-242-13360

Query Match
Best Local Similarity 25.0%; Score 332.5; DB 10; Length 259;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
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```
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 13360
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-815-242-13360

Query Match
Best Local Similarity 35.1%; Pred. No. 7.3e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

QY 15 ITGASGLGATARLVGQASAVLLDLPNSGGE-----QAQKRLGNNCFAPADYTS 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 ITGSSRGIGLAIARFQAQGANIVL---NSRGAISELLAEFSNGIKVVPISGDVSDF 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 69 KDVOATALAKKRGFRVDVAVNCAGIAVASKTYNLKKGTHLEDFORVLDVNLMTFNV 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 66 ADARKMDQARLAEIGSVDLVNNNGI--TQDTLTKM---TEADPEKVKVNLGTAFNM 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 IRLVAGEMGNPDGGRGVITINTASVAAPFEGVOGAAYSASKGIYGMTLPARDLAP 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 120 TQSVL-----KPMKAKREGAILIMSSVVGIMGICANTASRAGLIGFTKSVAREVAS 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 IGIVMTIAPLGFSTPLTSLPEKYNCFLASQVPPFSRLDPAFYAHVIAIENPFLNG 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 174 RNIYVNTIAPMISDMTALISDKIKRTAQIIPM-KEFGQAREVADLTVPFAGQVYLTG 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 EVIRLDGAIRM 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 233 QVIAIDGGLSM 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-09-815-242-13581
Sequence 13581, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlson, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 13581
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-815-242-13581

Query Match
Best Local Similarity 35.1%; Pred. No. 7.3e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
```

```

? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,931
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 13581
? LENGTH: 243
? TYPE: PRN
? ORGANISM: Streptococcus pneumoniae
US-09-815-242-13581

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Query Match	25.0%;	Score 326.5;	DB 10;	Length 243;
Best Local Similarity	35.1%;	Pred. No. 7.3e-22;		
Matches	88;	Conservative	36;	Mismatches 104;
				Indels 23;
				Gaps 6

[illegible]

```

RESULT 15
US-09-815-242-10921
Sequence 10921, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815_242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/255, 625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10921

```

```
; LENGTH: 245
; TYPE: PRF
; ORGANISM: Enterococcus faecalis
;
US-09-815-242-10921
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Query Match	24.4%;	Score 318.5;	DB 10;	Length 245;
Best Local Similarity	33.7%;	Pred. No. 3.9e-21;		
Matches 84; Conservative	38;	Mismatches 108;	Indels 19;	Gaps 5

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OY 15 ITGASGLGATIERIVGGOGASAVLDD-----LPNSGGGAOKKIGNNCVFAPADVSEKD 70
Db 10 ITGSTRIGKAAVLAFAKKGANIVLNGREITPEOROLETA--FGVKCIGLSGDISPDA 67
OY 71 VQATALAKKFKFRVAVAVANCAGIAVASKTYLKKGGTHTEDEFORVAVDVLMTFNVIR 130
Db 68 AGEMIGQATVQGLSIDILVNNAGIT-----NDKLLMTREDFNACDILNVGTFMNQ 121
OY 131 LVAGEMQONPDDGGGRGVITNTASAAPEGOGVGAASAASKGIGVGTLEIAPDLPIG 190
OY 122 QAKRKAMKQ-----KSGRIIMKASVSGLMGVGQANVAASKAGVGTCKVAEVAAPRG 175
Db 191 IRWVTIAPGLFGPILTSLPEKYCNFLAQVFFPSRLDDPAEYIAHLVATIEENPFLNGEV 250
Db 176 ITCNALPAGTQIOTEMTDLSEKVTOMNQIPLQTFQGEVDVAKTAIFELKSPFIITGOV 234
OY 251 TRUDGATRM 259
Db 235 VNVDGGLVM 243

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RESULT 16
US-10-175-696-14
; Sequence 14, Application US/10175696
; Publication No. US200300926588A1
GENERAL INFORMATION:
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Now, Laura A.
TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-193001
CURRENT APPLICATION NUMBER: US/10/175,696
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: 10/067,668
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/266,140
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/823,901
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/US01/10720
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/193,920
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/862,658
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: PCT/US01/16380
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/205,675
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/882,837
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: PCT/US01/19319
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/211,727
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 237
TYPE: PRT
ORGANISM: Homo sapiens
US-10-175-696-14
Query Match 24.1%; Score 314; DB 9; Length 237;

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Thu Jun 26 06:55:08 2003

us-09-931-186-4.rapb

Page 10

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; TYPE: PRT
; ORGANISM: Bacillus megaterium
; US-09-479-040-9

Query Match
Best Local Similarity 23.1%; Score 301; DB 9; Length 247;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

QY 7 SVKGLVAVITGASGLGATLAEKLVGQ-----ASAVLLDLPNSGGEAQA 53
DB 3 TLQKGAIVITGSGKIGALITRELSANGKAVANVNSKESAEAIYKEIKDNGEA 58
QY 54 LGNCFAPADYSEEDVGTALAKGKRGVDVAVNCAGIIVASKTYLTK-IGQTHILE 112
DB 59 -----IAVQADVSYDQAKHLIEETAAFGQDLIVNNAGI--TRDRSEFKLGE 106
QY 113 DEQRLVDVNLMTGFVNLVAVGEMGQNEPDGQGRGVIIINTASVAFEGVQAAYASAK 172
DB 107 DMKRVIVNLHSYNTTSAALFHLSE---GGR--VINISIIQAGGFGQTYNSAK 160
QY 173 GGVGVTLPIDRLAPIGIRVMTIAPGLTGTPLTSLPEKYNCFASQVFPFSRLGDPAE 232
DB 161 AGMLGFTKSLALBLATGVTVAICPGFETEKVMAIPEDVAKIVAKIP-TRRLGHAE 219
QY 233 YAH-LVQAIIEPFNGEVIKRLDGAIRM 259
DB 220 IARGVYVLAKDGAIVITGQQLNTINGLYM 247

RESULT 20
US-09-773-748-1
; Sequence 1, Application US/09773748
; Publication No. US20020187537A1
; GENERAL INFORMATION:
; APPLICANT: Wada, Masaru
; TITLE OF INVENTION: Levodione reductase gene and use thereof
; FILE REFERENCE: Levodione reductase
; CURRENT APPLICATION NUMBER: US/09/773,748
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: EP00101665.8
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Corynebacterium aquaticum
; US-09-773-748-1

Query Match
Best Local Similarity 22.5%; Score 293.5; DB 9; Length 267;
Matches 84; Conservative 45; Mismatches 98; Indels 37; Gaps 9;
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QY 12 VAVITGASGLGATLAEKLVGQASAVLLDLPNSGGEAQAQKLGNNCFAP-----ADVT 66
DB 15 VVLTITGSGSLGATLAEKLVGQASAVLLDLPNSGGEAQAQKLGNNCFAP-----ADVT 74
QY 67 SEDVGTALAKGKRGVDVAVNCAGIIVASKTYLTKKQTHLEDPQRLVDVNLMTGF 126
DB 75 DEQRLVDVNLMTGFVNLVAVGEMGQNEPDGQGRGVIIINTASVAFEGVQAAYASAK 129
QY 127 ----NVLIVAGEMGQNEPDGQGRGVIIINTASVAFEGVQAAYASAKSGIIVGTLPI 182
DB 130 LGLEKVLKIR-----EAGS--GMVYNTASVSGIRIGNSGYAAKHHGVGILRMS 179
QY 183 ARDLAPIGIRVMTIAPGLTGTPLTSL-----PEKYNCFASQVFPFSRLGDPAY 233
DB 180 AVEYGRGIRINLAIGALITRELSANGKAVANVNSKESAEAIYKEIKDNGEA 237
QY 234 AHLVQAIIE--PFLNGEVIKRLD 255
DB 238 AAVYAFLLSDASVAVNATVYPIDG 261
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RESULT 21
US-10-307-385-6
; Sequence 6, Application US/10307385
; Publication No. US20030077797A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; TITLE OF INVENTION: XYLILOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/10/307,385
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US/09/363,189
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: JP10-216047
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Gluconobacter oxydans
; US-10-307-385-6

Query Match
Best Local Similarity 22.4%; Score 292.5; DB 9; Length 262;
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;
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QY 6 RSVKGLVAVITGASGLGATLAEKLVGQASAVLLDLPNSG---GEAQAQKLGNNCFAP 62
DB 3 KFNKGVCLVITGAGGNIATLALRLAEGGTALIDMKREALEKASVREKGEARSYV 62
QY 63 ADVTSEKVPQALALAKKRGVDVAVNCAGIIVASKTYLTKKQTHLEDPQRLVDVNL 122
DB 63 CDVTESEAVITGVDSVVDGKIDPLFNNAIQCA-----FAPVDDPSDFARVLIIV 117
QY 123 MGFENVIRLVAGEM-GQNEPDGQGRGVIIINTASVAFEGVQAAYASAKSGIIVGTLPI 181
DB 118 TGAFFVHLKAVSRQMTQN-----YGRIVNTASVAGVGPNNAAAGASGALITALET 170
QY 182 IARDLAPIGIRVMTIAPGLTGTPLTSLPEKYNCFASQVFPFSRLGDPAY 225
DB 171 AALDLAPINIRYNALSPGIMPGGEMERQVELQAKVSGQYSTDPRKYVAQOMISGVPR-R 229
QY 226 RLGDPAEYAHVQAIIE--ENPFLNGEVIKRLD 255
DB 230 RYGDINEIPGVAVFLIGDSSFMGMVNPING 261
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RESULT 22
US-09-802-853-6
; Sequence 6, Application US/09802853
; Patent No. US20010034049A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; TITLE OF INVENTION: XYLILOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/09/802,853
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/363,189
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: JP10-216047
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PRT
```

ORGANISM: Gluconobacter oxydans  
US-09-802-853-6

Query Match 22.4%; Score 292.5; DB 10; Length 262;  
Best Local Similarity 31.6%; Pred. No. 9, 6e-19;  
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

QY 6 RSVKGLVAVITGASGLGATATERYLVGGASAVLDLPNSG--GPAQKTKLGNVCVAF 62  
DB 3 KKEKNGVCLVTGAGGIGLATALRLAEETALALDMDNEALEKAEASVREKGVARSV 62  
QY 63 ADYTSKDVQIALALAKKFGRYDAVAVNCAGIAVASKTYNLKGGTHLTEDFORVLDVNL 122  
DB 63 CDVTSEAVIGIVDSVVRDFGKIDFLFNAGYOGA----FAPVDYPSDDPFRVLTIV 117  
QY 123 MGFENYIRLVAGEM-GQNEPDQGGRGVITINTASVAFEGVGOAAYSASKGIYGMTLP 181  
DB 118 TGAFTVLKAVSRMTQN-----YGRIVNTRASNAGVGPNNMAAYGSKAIIALTET 170  
QY 182 IARDLAPIGIRVNTIAPGLF-----GTEPLTSLPEKYCNFIASQVPPPS 225  
DB 171 AALDLAPYINRYVAISFGYMGSGFMWRQVELQAKVGSYFSTDPVVAQOMIGSVPM-R 229  
QY 226 RLGDPPEVAHLVQAII--ENPFLNGEIVRLDG 255  
DB 230 RYGDINEIPGVVAFELGDDSSFTGTGNLPIAG 261

## RESULT 23

US-09-978-295A-468  
Sequence 468, Application US/09978295A  
Patent No. US20020156006A1

GENERAL INFORMATION:  
APPLICANT: Asinhenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: F2630PIC11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
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PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819

Thu Jun 26 06:55:08 2003

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Page 12

PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
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PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
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PRIOR FILING DATE: 1998-05-06  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
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PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.4%; Score 291.5; DB 9; Length 270;  
Best Local Similarity 31.7%; Pred. No. 1.2e-18;  
Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

QY 1 MAAVRSVKGLVAVITGASGLATAEPLVGOGASAVLILPNSGGEQAKKGNVCF 60  
DB 1 MATGER-YAKGVYVYVGGGIGAGIVRAFVNSGARVYIDCKDSGRLAECEL-DGAYF 58  
QY 61 APADYSEKDYORALAKGKFGRVYAVVACAGIYASAKYINLKQOTHTLEDFORYLDV 120  
DB 59 ILCDVTGEDVDKVLVSETIRFGRLDCVNNAGHPPP-----QREETSAGFROLLEL 113  
QY 121 NMGTFVIVILVAGEMQNEPDGQGRVYIINTASVAEFQYGOAAYSASKGIYGMTL 180  
DB 114 NLSTYTLTKLALPYLRKSQ-----GNVINISLVGAIGQAVPYATKGAVTAMRK 166  
QY 181 PIARDLPICIRWTIAPGFGTPILTSLPEKYNFLASQVPP-----SRL 227  
DB 167 ALADESPYGVKVCISPGNIWTPLMEE-----LAALMPDRAIRIRGMLAQPLGRM 218  
QY 228 GDPAEY-AHLVOATIEHPFLNG-EVIRLDGA 256  
DB 219 GQPAEYGAANVFLASEANFCTGIELLVYTGGA 249

RESULT 24  
US-09-978-697-468  
Sequence 468, Application US/09978697  
Parent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: ASHKENAZI, AVI  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Girdlens, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, Timothy A.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978,697



1	CURRENT FILING DATE: 2001-10-16
2	PRIOR APPLICATION NUMBER: 09/918585
3	PRIOR FILING DATE: 2001-07-30
4	PRIOR APPLICATION NUMBER: 60/063250
5	PRIOR FILING DATE: 1997-10-17
6	PRIOR APPLICATION NUMBER: 60/064249
7	PRIOR FILING DATE: 1997-11-03
8	PRIOR APPLICATION NUMBER: 60/065311
9	PRIOR FILING DATE: 1997-11-13
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11	PRIOR FILING DATE: 1997-11-21
12	PRIOR APPLICATION NUMBER: 60/077450
13	PRIOR FILING DATE: 1998-03-10
14	PRIOR APPLICATION NUMBER: 60/077632
15	PRIOR FILING DATE: 1998-03-11
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21	PRIOR FILING DATE: 1998-03-12
22	PRIOR APPLICATION NUMBER: 60/078004
23	PRIOR FILING DATE: 1998-03-13
24	PRIOR APPLICATION NUMBER: 60/078886
25	PRIOR FILING DATE: 1998-03-20
26	PRIOR APPLICATION NUMBER: 60/078936
27	PRIOR FILING DATE: 1998-03-20
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29	PRIOR FILING DATE: 1998-03-20
30	PRIOR APPLICATION NUMBER: 60/078939
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34	PRIOR APPLICATION NUMBER: 60/079556
35	PRIOR FILING DATE: 1998-03-26
36	PRIOR APPLICATION NUMBER: 60/079664
37	PRIOR FILING DATE: 1998-03-27
38	PRIOR APPLICATION NUMBER: 60/079689
39	PRIOR FILING DATE: 1998-03-27
40	PRIOR APPLICATION NUMBER: 60/079663
41	PRIOR FILING DATE: 1998-03-27
42	PRIOR APPLICATION NUMBER: 60/079728
43	PRIOR FILING DATE: 1998-03-27
44	PRIOR APPLICATION NUMBER: 60/079786
45	PRIOR FILING DATE: 1998-03-27
46	PRIOR APPLICATION NUMBER: 60/079920
47	PRIOR FILING DATE: 1998-03-30
48	PRIOR APPLICATION NUMBER: 60/079923
49	PRIOR FILING DATE: 1998-03-30
50	PRIOR APPLICATION NUMBER: 60/080105
51	PRIOR FILING DATE: 1998-03-31
52	PRIOR APPLICATION NUMBER: 60/080107
53	PRIOR FILING DATE: 1998-03-31
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56	PRIOR APPLICATION NUMBER: 60/080194
57	PRIOR FILING DATE: 1998-03-31
58	PRIOR APPLICATION NUMBER: 60/080327
59	PRIOR FILING DATE: 1998-04-01
60	PRIOR APPLICATION NUMBER: 60/080328
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62	PRIOR APPLICATION NUMBER: 60/080333
63	PRIOR FILING DATE: 1998-04-01
64	PRIOR APPLICATION NUMBER: 60/080334
65	PRIOR FILING DATE: 1998-04-01
66	PRIOR APPLICATION NUMBER: 60/081070
67	PRIOR FILING DATE: 1998-04-08
68	PRIOR APPLICATION NUMBER: 60/081049
69	PRIOR FILING DATE: 1998-04-08
70	PRIOR APPLICATION NUMBER: 60/081071
71	PRIOR FILING DATE: 1998-04-08
72	PRIOR APPLICATION NUMBER: 60/081195
73	PRIOR FILING DATE: 1998-04-08

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Page 14

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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.4%; Score 291.5; DB 9; Length 270;  
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Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

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181 PIADLPIGIRVITAPGLFGLPLTSLPEKVCNFIASQVPP-----SRL 227  
167 ALADESPYGVYVNCISPGNTWPLME-----LAALMPDPRATIRGMLAQPLGRM 218  
228 GDPAEY-AHLVQAIENPFLNG-EVIRLDGA 256  
219 GQPAEVGAAMVFLASEANFCIGIELVTGGA 249

RESULT 25  
US-09-978-192A-468  
Sequence 468, Application US/09978192A  
Patent No. US2002017553A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C9  
CURRENT FILING DATE: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
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PRIOR FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.4%; Score 291.5; DB 9; Length 270;  
Best Local Similarity 31.7%; Pred. No. 1.2e-18;  
Matches 86; Conservative 42; Mismatches 106; Indels 37; Gaps 8;

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RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogatawara N., Moszer I., Albertini A.M., Alloni G.,
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RA Borris R., Bourcier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Ertan K.D., Erlington J., Fabret C., Ferrazi E., Fougere D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gilm S.T., Glaser P., Goffeau A., Golightly E.T., Grandi G.,
RA Guisepi H., Guy B.J., Haga K., Halech J., Harwood C.R., Henauf A.,
RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Ilaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapides A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Paro V., Pohl T.M., Portetelle D., Portwille S., Prescott A.M.,
RA Prescan E., Pujic P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccoti E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Taccoti E., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi V., Uchiyama S., Vandendol M., Vanlier F., Vasseroiti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzneger T.,
RA Winters P., Wiput A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zumbstein A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
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RT Nature 390:249-256(1997)
CC - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC -----
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DR HSP: P50162; IAE1.
DR Subtilisin; BGI0628; ywFD.
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DR Pfam: PF00106; adh_short.1.
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DB 71 HAVESAVHTFGDLVNLNAGIELVAPHEHE-----LSMKNVLYQVNLGTMKXHA 124
OY 131 ---LVAGEMQNEPDGQGRGVLIINTASVAAFEGVQAAYSAKSGIVGMLPIARDL 186
DB 125 LKHMLAAG-----KGNIIITCSVGLVAMPDIPAYNASKGSGVLDLITKSMADV 172

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OY 234 AHLVQAITE--NPLNGEVIRLDCAIMQ 260
DB 227 ANVMLFLASDLSYMTGSATTAQDGVTAAQ 255
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DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
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RA Marekov L., Krook M., Joernvall H.;
RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
RT 'short-chain, non-metalloenzyme' alcohol dehydrogenase type.";
RL FEBS Lett. 266:51-54(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RA MEDLINE=92052211; PubMed=1946424;
RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
RA Rimsay R.L., Orr J.C.;
RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
RT dehydrogenase: a member of a short-chain dehydrogenase family.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
CC - CATALYTIC ACTIVITY: Androstane-3-alpha,17-beta-diol + NAD(+) = 17-
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DR PDB: 1HDC; 07-FEB-95.
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DB 169 ELGTDRIRVNSVHPGKTYTPMAETGIRQEGNT--PNTPM-GRVQNEFGELTAGAVYKLL 225

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 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
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 RP MEDLINE-97305956; PubMed-9163424;  
 RA Freiderg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,  
 RA Perret X.;  
 RT "Molecular basis of symbiosis between Rhizobium and legumes."; a  
 RL Nature 387:394-401(1997).  
 RN [2]  
 RP MEDLINE-96389014; PubMed-8796346;  
 RA Freiderg C., Perret X., Broughton W.J., Rosenthal A.;  
 RT "Sequencing the 500-kD GC-rich symbiotic replicon of Rhizobium sp.  
 NGR234 using dye terminators and a thermostable 'sequenase'"; a  
 RL Genome Res. 6:590-600(1996).  
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY. CONTAINS TWO DOMAINS.

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DR EMBL: Z68203; CA92424.1; AUT\_INIT.  
 DR EMBL: AE000101; AAB91897.1; .  
 DR HSSP: P50163; ZAE1.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 2.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 KW Hypothetical protein; Oxidoreductase; Plasmid; Repeat;  
 KW Multifunctional enzyme.  
 KM DOMAIN 1 250  
 FT DOMAIN 1 250  
 FT NP\_BIND 12 548  
 FT NP\_BIND 12 37  
 FT ACT\_SITE 154 154  
 FT ACT\_SITE 280 304  
 FT NP\_BIND 280 304  
 FT ACT\_SITE 420 420  
 FT ACT\_SITE 420 420  
 SQ SEQUENCE 548 AA; 57593 MM; 399598C5DF17C23F CRC64;

Query Match 22.6%; Score 294.5; DB 1; Length 548;  
 Best Local Similarity 33.6%; Pred. No. 1.3e-15;  
 Matches 86; Conservative 41; Mismatches 100; Indels 29; Gaps 8;

QY 10 GIVAVITGGASGIGTAERTVGOGASAVILDPNNGGGAOKKIGNOVFPAPDYTSK 69  
 DB 9 GRIIVVIGAGGIGRGLVDFPANGGVYVAVDLPDSGVLELGNLDEPHIGLEVDSRD 68

QY 70 DVQATIALAKGKGRGVAVNACGI---AVASKTYNLKKGQTHLLEDFQVRLVDVLMGT 125  
 DB 69 DVVALRALLEKRSRIEVLVNNMGIGFTMAATADT-----ALEDFQALATLVGA 119

QY 126 FNVIRLVAGMGONEPDQGGRGVITINTASVAFEGOVGAAYASAKSGIYGTLPARD 185  
 DB 120 YSVACETAKLM---KRG-----AIVNVAISLGLGNPKRSAYASAKSAGLITTKSLAR 171

QY 186 LAPIGIRVMTIAPGLFTPLTSLPERV---CNFLASQVFPSPRLGDPAEYAHLYO--A 239  
 DB 172 MASRGIVRTAVAPGHVTRPVAVEL-ERAGKLDVSAIRRVPL-GRIRAPDEIARAVRFLA 229

QY 240 IIEPPELNGEYIRLDG 255  
 DB 230 SAQASYTTGSTLVVDG 245

RESULT 18  
 BA7L\_EUBSP STANDARD: PRT: 249 AA.

ID BA7L\_EUBSP STANDARD: PRT: 249 AA.  
 AC P07914;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) (Bile acid  
 DE 7-dehydroxylase) (7-alpha-HSDH) (Bile acid-inducible protein).  
 GN BA7A1 AND BA7A3.  
 OS Eubacterium sp. (strain VPI 12708).  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=29347;  
 RN [1]  
 RP MEDLINE-9030548; PubMed-2375653;  
 RA Gopal, Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.;  
 RT "Multiple copies of a bile acid-inducible gene in Eubacterium sp.  
 strain VPI 12708."; a  
 RL J. Bacteriol. 172:4420-4426(1990).  
 RN [2]  
 RP MEDLINE-86197993; PubMed-2834320;  
 RA Coleman J.P., White W.B., Lilewski M., Hylemon P.B.;  
 RT "Nucleotide sequence and regulation of a gene involved in bile acid  
 RT 7-dehydroxylation by Eubacterium sp. strain VPI 12708."; a  
 RL J. Bacteriol. 170:2070-2077(1988).  
 RN [3]  
 RP MEDLINE-97165759; PubMed-3549693;  
 RA Coleman J.P., White W.B., Hylemon P.B.;  
 RT "Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp.  
 strain VPI 12708."; a  
 RL J. Bacteriol. 169:1516-1521(1987).  
 CC -1 FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID, YIELDING  
 CC DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST  
 CC AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID.  
 CC -1 CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-  
 CC cholanate + NAD(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-  
 CC cholanate + NADH;  
 CC -1 PATHWAY: Bile acid catabolism.  
 CC -1 INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A  
 CC 7-ALPHA-HYDROXY GROUP.  
 CC -1 SIMILARITY: THERE ARE THREE GENES FOR BAI1 PROTEINS: BAI1 IS  
 CC IDENTICAL TO BAI3 AND THERE IS 81% IDENTITY WITH BAI2.  
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.

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DR EMBL: M34658; AAB61155.1; .  
 DR EMBL: M19654; AAB61154.1; .  
 DR EMBL: M15813; AAB61153.1; .





DT 01-OCT-1994 (Rel. 30, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE OXidoreductase ucpa (EC 1.1.1.177).  
 OS ucpa OR STM2445 OR STY2682.  
 GN Salmonella typhimurium, and  
 OS Salmonella typhimurium, and  
 OC Salmonella typhimurium.  
 OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC NCBI\_Taxid=602, 601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 RT LT2.";  
 RN Nature 413:852-856(2001).  
 RL [2]  
 RP SEQUENCE OF 204-263 FROM N.A.  
 RC SPECIES=S.typhimurium;  
 RX MEDLINE=91358382; PubMed=1909324;  
 RA Hryniewicz M.M., Kredich N.M.;  
 RT "The cyst promoter of *Salmonella typhimurium*: characterization of two  
 RT binding sites for CysB protein, studies of in vivo transcription  
 RT initiation, and demonstration of the anti-inducer effects of  
 RT thiosulfate.";  
 RL J. Bacteriol. 173:5876-5886(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.typhimurium;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebalina M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jorgels K.,  
 RA Kooch A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrett B.G.;  
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*  
 RT enterica serovar Typhimurium CT18.";  
 RL Nature 413:848-852(2001).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AE008810; AAL21339.1; -  
 DR EMBL: AL627274; CAD07676.1; -  
 DR PIR: A38121; A38121.  
 DR STyGene; SG10424; ucpa.  
 DR InterPro: IPR002198; ADH\_short.  
 DR PROSITE: PS00061; ADH\_SHORT; FALSE\_NEG.  
 KW Oxidoreductase; Complete proteome.  
 FT CONFLICT 218 L-> M (IN REF. 2).  
 FT CONFLICT 258 S-> T (IN REF. 2).  
 FT CONFLICT 263 V-> I (IN REF. 2).  
 FT SEQUENCE 263 AA; 27870 MM; 81B26CAD9BD4534E CRC64;  
 SQ  
 Query Match 22.1%; Score 288; DB 1; Length 263;  
 Best Local Similarity 32.2%; Pred. No. 1,8e-15;  
 Matches 85; Conservative 38; Mismatches 105; Indels 36; Gaps 8;

QY 10 GLVAVITGASGLGATAEKRYVGOGASAVLLDLPNSGGEAOKL-----GNNGVEAP 62  
 Db 6 GKTLALITGASGIEGIAFYARFARGANILLIDISD-----EIEKLADELGRGRHCAVX 60  
 QY 63 ADVTSEKDVQATALAKRGEGVDVAVNAGIAVASTYLNKKGQTHLTDFORVLDVNT 122  
 Db 61 ADVADPASFVQAARARAKETEGRIDILVNNAGVCLGNFLDMSK-----EDRDFRIDINI 114  
 QY 123 MGTENVIRPLVAGEKQNPDDGGQGVYIINTASTAA-FEGVGAASASKGGIVGKTLR 181  
 Db 115 KGVNWTAKVLPKEMIKRD-----GRIVMSSVTGDMVADPGSTAAALSKAIVGLTKS 168  
 QY 182 IARDLAPIGIRVMTIAPGLFGTPLLTSV-----PEKVCNPLASQVPPSPRLGDAEY 233  
 Db 169 LAVERAAGSIRVNNACPGYVRTPMASIAARQNDDESVLTAKAKIPL-RLADPLEV 227  
 QY 234 AHLVQ-AIENPFLNGEVIRLDG 255  
 Db 228 GELAAFLASDESSYLTGTQNVIDG 251  
 RESULT 23  
 PHBB\_ALCEU STANDARD; PRT; 246 AA.  
 ID P14697;  
 AC 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Acetoacetyl-CoA reductase (EC 1.1.1.36).  
 GN PHBB.  
 OS Alkaliigenes eutrophus (Ralstonia eutropha).  
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;  
 OC Ralstonia.  
 OC NCBI\_Taxid=510;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H16 / DSM 428 / ATCC 17699;  
 RX MEDLINE=89559356; PubMed=2670935;  
 RA Peoples O.P., Sinskey A.C.;  
 RT "Poly-beta-hydroxybutyrate biosynthesis in Alkaliigenes eutrophus H16.  
 RT Characterization of the genes encoding beta-ketothiolase and  
 RT acetoacetyl-CoA reductase.";  
 RL J. Biol. Chem. 264:15293-15297(1989).  
 CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) = 3-oxoacyl-CoA + NADPH.  
 CC -1- PATHWAY: Poly-beta-hydroxybutyrate biosynthesis; second step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: J04987; AAA21973.1; -  
 DR PIR: B34340; KDAIAE.  
 DR HSP; 070351; 1B3S.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR PRINTS: PR00080; SDRFAMILY.  
 DR PROSITE: PS00061; ADH\_SHORT; 1.  
 KW Oxidoreductase; NADP; PHB biosynthesis.  
 FT NP\_BIND 8 NADP (BY SIMILARITY).  
 FT ACT\_SITE 153 BY SIMILARITY.  
 FT SEQUENCE 246 AA; 26370 MM; AD6739E0F5C93C06 CRC64;  
 SQ  
 Query Match 22.0%; Score 287.5; DB 1; Length 246;  
 Best Local Similarity 31.9%; Pred. No. 1,8e-15;





DR PRINTS: PRO0080; SDRFAMILY  
DR PROSITE; PS00061; ADH\_SHORT. 1.  
RW Hypothetical protein; Oxidoreductase; NADP (By Similarity).  
FT NP\_BIND 9 33  
FT ACID\_SITE 153 153  
FT ACID\_SITE 130 136  
FT COMPILOT 256 AA; 28078 MW; D61601D1798006B CRCC4;  
SQ SEQUENCE

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:23:47 ; Search time 15.6667 Seconds

(without alignments)  
1601.559 Million cell updates/sec

Title: US-09-931-186-4

Perfect score: 1304  
Sequence: 1 MAAAVRSVKGLVAVITGGAS.....ENPFLNGEYIRLDGAIKMPD 261

Scoring table: BLASTX62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	750	57.5	258	2 T20484	hypothetical prote
2	720	55.2	255	2 H83326	probable short-cha
3	711	54.5	255	2 AG3611	3-oxoacyl-(acyl-ca
4	671.5	51.5	250	2 A70554	probable dehydroge
5	670	51.4	255	2 H95360	probable imported
6	642	49.2	257	2 F97531	probable short-cha
7	642	49.2	257	2 AG2750	3-hydroxyacyl-CoA
8	595	45.6	260	2 C87264	3-oxoacyl-(acyl-ca
9	383.5	29.4	247	2 E70740	probable fabG2 pro
10	355	27.2	252	2 F83098	probable short-cha
11	343.5	26.3	249	2 F97338	3-ketoacyl-acyl ca
12	341	26.2	246	2 H72219	3-oxoacyl-(acyl ca
13	336.5	25.8	297	2 T51084	3-oxoacyl-(acyl-ca
14	334	25.6	320	2 S22450	3-oxoacyl-(acyl-ca
15	333.5	25.6	246	2 C83961	3-oxoacyl-(acyl-ca
16	333.5	25.6	251	2 AH2042	3-oxoacyl-(acyl-ca
17	332	25.5	246	2 H84136	3-oxoacyl-(acyl-ca
18	328.5	25.2	248	2 F8128	3-oxoacyl-(acyl-ca
19	326.5	25.0	243	2 E97919	3-oxoacyl-(acyl-ca
20	325.5	25.0	243	2 G95048	3-oxoacyl-(acyl-ca
21	324.5	24.9	243	2 G95048	3-oxoacyl-(acyl-ca
22	317	24.3	299	2 D80481	hypothetical prote
23	315.5	24.2	260	1 A48134	hypothetical prote
24	315.5	24.2	260	1 T36846	short-chain alcoh
25	315	24.2	267	2 T11579	probable dehydroge
26	314.5	24.1	259	2 H98137	probable short cha
27	314.5	24.1	259	2 H98137	3-oxoacyl-(acyl-ca
28	313.5	24.0	240	2 H75014	3-oxoacyl-(acyl-ca
29	313.5	24.0	247	2 S77280	3-oxoacyl-(acyl-ca

30	312.5	24.0	296	2 E87260	hypothetical prote
31	311	23.8	247	2 F82776	3-oxoacyl-(acyl) re
32	311	23.8	262	2 AB3545	3-oxoacyl-(acyl) re
33	309.5	23.7	244	2 AB0195	3-oxoacyl-(acyl-ca
34	309.5	23.7	246	2 A69621	3-oxoacyl-(acyl-ca
35	309	23.7	249	2 AG3121	dehydrogenase Atu4
36	309	23.7	253	2 H98165	3-oxoacyl-(acyl-ca
37	306	23.5	256	2 A10406	probable dehydroge
38	305	23.4	260	2 H70758	probable fabG3 pro
39	303.5	23.3	247	2 AG1300	3-oxoacyl-acyl ca
40	303	23.2	248	2 H98258	3-oxoacyl-(acyl-ca
41	303	23.2	248	2 A13025	3-oxoacyl-(acyl-ca
42	301.5	23.1	247	2 AG1672	3-ketoacyl-acyl ca
43	301	23.1	255	1 S39377	glucose 1-dehydrog
44	300.5	23.0	256	1 T26723	hypothetical prote
45	300	23.0	250	1 S47054	probable dehydroge
46	300	23.0	255	1 S10707	20beta-hydroxyster
47	298	22.9	252	2 B90495	hypothetical prote
48	296.5	22.7	258	2 C70885	probable dehydroge
49	296	22.7	245	2 AE3517	3-oxoacyl-(acyl-ca
50	294	22.5	255	2 H84288	3-oxoacyl-(acyl-ca
51	294	22.5	255	2 T36596	probable short cha
52	293	22.5	249	1 B37762	bile acid 7-dehydr
53	291.5	22.4	249	1 T12051	3-oxoacyl-(acyl-ca
54	291	22.3	258	2 D95284	probable imported
55	290.5	22.3	248	2 H70447	3-oxoacyl-(acyl-ca
56	290	22.2	272	2 AG3359	glucose 1-dehydrog
57	289.5	22.2	244	1 B42147	3-oxoacyl-(acyl-ca
58	288	22.1	253	2 AB0812	probable oxidoredu
59	287.5	22.0	266	1 RDALAE	acetoacetyl-CoA re
60	287.5	22.0	303	2 T46064	short-chain alcoh
61	286.5	22.0	244	2 G90812	3-oxoacyl-(acyl-ca
62	286.5	22.0	244	2 C85672	3-oxoacyl-(acyl-ca
63	285.5	21.9	254	2 G75333	3-oxoacyl-acyl-car
64	285	21.9	255	2 G82644	2,5-dichloro-2,5-c
65	284.5	21.8	256	2 E72427	oxidoreductase, sh
66	284.5	21.8	257	2 A72395	oxidoreductase, sh
67	283.5	21.7	244	2 AD0642	3-oxoacyl-(acyl-ca
68	283.5	21.7	253	2 B86737	acetoin dehydrogen
69	283.5	21.7	232	2 A99950	hypothetical prote
70	282.5	21.6	251	2 C87474	hypothetical prote
71	282	21.6	255	2 D72377	oxidoreductase, sh
72	281.5	21.6	246	1 DEKNG	acetoacetyl-CoA re
73	279.5	21.4	241	1 S06998	acetoacetyl-CoA re
74	279.5	21.4	248	1 E81695	3-oxoacyl-(acyl ca
75	279	21.4	240	2 F87312	acetoacetyl-CoA re
76	279	21.4	258	2 B89773	acetoin(diacetyl)r
77	278	21.3	262	2 B97588	oxidoreductase, sh
78	278	21.3	262	2 AG2809	short chain dehydr
79	277.5	21.3	289	2 D69825	glucose 1-dehydrog
80	277	21.2	260	2 F82954	probable short-cha
81	276	21.2	249	1 A31841	bile acid dehydrox
82	276	21.2	285	1 A65017	probable 3-oxoacyl
83	276	21.2	285	2 A91041	probable oxidoredu
84	276	21.2	319	2 D85885	3-oxoacyl-(acyl-ca
85	276	21.2	248	2 S22416	3-oxoacyl-(acyl-ca
86	275.5	21.1	248	2 T43361	acetoacetyl-CoA re
87	275	21.1	246	1 S29279	acetoacetyl-CoA re
88	275	21.1	267	2 B87578	hypothetical prote
89	274.5	20.9	248	2 B97223	probable 3-ketoacy
90	272.5	20.9	244	2 T44434	3-oxoacyl-(acyl-ca
91	272.5	20.9	286	2 G83378	probable short-cha
92	272	20.9	251	2 G72389	oxidoreductase, sh
93	272	20.9	259	2 E95903	probable dehydroge
94	272	20.9	263	2 S01227	glucose 1-dehydrog
95	270.5	20.7	240	2 S75021	3-ketoacyl-acyl ca
96	270.5	20.7	248	2 F71538	probable oxoacyl (
97	270.5	20.7	262	2 D97325	3-oxoacyl-acyl car
98	270.5	20.7	268	2 A66378	protein F2109.2 [1
99	270	20.7	308	2 G96016	probable gluconat
100	269.5	20.7	246	2 B89896	3-oxoacyl-(acyl-ca









N:Alternate names: protein B2A19.180  
 C:Species: Neurospora crassa  
 C>Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 24-May-2001  
 C:Accession: T51084  
 R:Schulze, U.; Aisp, V.; Hohnsiedel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000  
 A:Reference number: 225286  
 A:Accession: T51084  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-297 <SCH>  
 A:Cross-references: EMBL:AL390092; GSPDB:GN00116; NCSP:B2A19.180  
 A:Experimental source: EAC clone B2A19; strain OR74A  
 C:Genetics:  
 A:Gene: NCSP:B2A19.180  
 A:Map position: 6  
 A:Introns: 218/1; 249/1  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.8%; Score 336.5; DB 2; Length 297;  
 Best Local Similarity 31.6%; Pred. No. 4.9e-19;  
 Matches 97; Conservative 40; Mismatches 103; Indels 67; Gaps 8;

OY 5 VRSVKGIVAVITGGASGLIATAEELVGGASAVLIDLPNS-----GGEA 49  
 DB 1 MRLSLHKOALITGGSGIGLAIARLYEGCVTLTGRTSTLQASQSLLSQPLHSPA 60  
 OY 50 CAKRLGNVCVAPADVSEKDVQAL-ALAKGRGVAVNVCAGIYAS---KTYLKK 105  
 DB 61 QPSPDKRVSTHPLNVTSSASSWEDLQNSKGGKGRVDILNCAGITQPSLMKT----- 115  
 OY 106 GQHTLEDFQVPLDVNLGTPNVIRLVAGENGQNEP-----DOGG----- 145  
 DB 116 ---SIEVEGLDPTNLKGLVIGCKFVGRAMLRNPSSQHPRVKADSGAGVGEETEE 171  
 OY 146 -----QGRVITNTASVAFAEGVQQAAYASAKGIVGKTLPIADLAPIG 190  
 DB 172 KGEGKGQGVREGVQERGVIIIVASLAKQKGVITSTVYAAKAGVGLTSLAHEGRSG 231  
 OY 191 IRVMTIAPGLFGTPLLTLSPKVCNFTLASQVPPFSRLDPAEYHVLVOAITENPFLGVEY 250  
 DB 232 IRVNAVLPGYIETDWTITLKNP---SILQQLPL-GREGTTEVADALFLIKNPYANNVCY 287  
 OY 251 IRLDGAI 257  
 DB 288 LNLDSGL 294

RESULT 14  
 3-oxoacyl-(acyl-carrier-protein) reductase (EC 1.1.1.100) precursor, NADPH-dependent [va  
 S22450  
 N:Alternate names: beta-ketoacyl-ACP reductase  
 C:Species: Cuphea lanceolata  
 C>Date: 16-Feb-1995 #sequence\_revision 23-Feb-1996 #text\_change 17-Mar-2000  
 C:Accession: S22450; S19832  
 R:Klein, B.; Pavlovski, K.; Hoerlicke-Grandpierre, C.; Schell, J.; Toepfer, R.  
 Moll. Gen. Genet. 233, 122-128, 1992  
 A:Title: Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta  
 A:Reference number: S22450; MUID:92293104; PMID:1376402  
 A:Accession: S22450  
 A:Molecule type: mRNA  
 A:Residues: 1-320 <KLE>  
 A:Cross-references: EMBL:X64566; NID:q18045; PIDN:CAA45866.1; PID:q18046  
 A:Experimental source: immature embryo  
 C:Genetics:  
 A:Gene: Ctkr27  
 A:Gene: nuclear  
 A:Function:  
 A:Description: EC 1.1.1.100 [validated, MUID:92293104]  
 A:Pathway: fatty acid biosynthesis  
 A>Note: Integral part of the fatty acid synthase type II  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
 C:Keywords: chloroplast; fatty acid biosynthesis; NADP; oxidoreductase

F:1-63/Domain: transit peptide (chloroplast) #status predicted <TNP>  
 F:64-320/Product: 3-oxoacyl-(acyl-carrier-protein) reductase #status predicted <NAT>  
 F:78-258/Domain: short-chain alcohol dehydrogenase homology <SADH>  
 F:227/Active site: Tyr #status predicted

Query Match 25.6%; Score 334; DB 2; Length 320;  
 Best Local Similarity 32.7%; Pred. No. 8.4e-19;  
 Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;

OY 2 AAARSVKGIIVAVITGGASGLIATAEELVGGASAVLIDLPNSGGEA-----QAKLGN 56  
 DB 69 AGAGGVSESPVIVITGASGIGALILSL-GRAGCVLVNVRSSKEAEVSEKELEARGG 127  
 OY 57 NCYFAPADVTSEKDVQALALAKKGRGVAVNVCAGIYASKTYNKKGQHTLEDQR 116  
 DB 128 QALTFFGDVSKEDVEMKRTAVDAGTVDLVNNAGITRDGLNEMKRSQ-----WQE 181  
 OY 117 VLDVNLGTFNVIRLVAGENGQNEPQGGVITNTASVAFAEGVQQAAYASAKGIV 176  
 DB 182 VIDNLNLTGVLCTQAAKIMMK-----KKGRITIASVGLVGNAGANYSAAKAGVI 235  
 OY 177 GMTPLPARDIAPICIRVMTIAPGLFGTPLLTLSPKVCNFTLASQVPPFSRLDPAEYHNL 236  
 DB 236 GFRTYAREVYASRNINAVAPGFISSDMTSLKLDINKRIETIPL-GRYQPEVAVGL 294  
 OY 237 VOAITENP---PLNGEYIRLDGAI 259  
 DB 295 VERFLAINPASVYTGQVFTIDGNTM 320

RESULT 15  
 3-oxoacyl-(acyl-carrier protein) reductase fabg [imported] - Bacillus halodurans (st  
 C83961  
 C:Species: Bacillus halodurans  
 C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 03-Aug-2001  
 C:Accession: C83961  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans  
 A:Reference number: A83650; MUID:20512582; PMID:11058132  
 A:Accession: C83961  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-246 <STO>  
 A:Cross-references: GB:AF001515; GB:BA000004; NID:q10174886; PIDN:BAB06210.1; GSPDB:  
 A:Experimental source: strain C-125  
 C:Genetics:  
 A:Gene: fabg  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.6%; Score 333.5; DB 2; Length 246;  
 Best Local Similarity 34.2%; Pred. No. 6.6e-19;  
 Matches 90; Conservative 42; Mismatches 102; Indels 29; Gaps 7;

OY 8 VKGLIVAVITGGASGLIATAEELVGGASAVLIDLPNSGGEA-----QAKLGNVCY 59  
 DB 2 LGKTAIVTASGIGRATIMELARIGANVY---NYAGNKEKAEKVVAEIKELGVEAI 57  
 OY 60 FAPADVTSEKDVQALALAKKGRGVAVNVCAGIYASKTYNKKGQHTLEDQR 119  
 DB 58 AIGADVADSESVQAMVETIDTGGAVDILVNNAGITRDGLNEMKRSQ-----EDMDAYVD 111  
 OY 120 VNLGTFNVIRLVAGENGQNEPQGGV-GVITNTASVAFAEGVQQAAYASAKGIV 178  
 DB 112 TNLKGVTHCKATYRPMK-----QGRRIITNVSSVGLINAGANVYAAKAGVIGL 164  
 OY 179 TLPARDIAPICIRVMTIAPGLFGTPLLTLSPKVCNFTLASQVPPFSRLDPAEYHNL 238  
 DB 165 TKTLARLARINNTVNVAVAPGFITDWTIGELPEDVYAKMLGQIPL-ARLQPEVAVAKAVR 223  
 OY 239 ALLEN--PFLNGEYIRLDGAI 259  
 DB 224 FLASDDASVLTGLTIHVNGKVM 246



RESULT 16  
3-oxoacyl-[acyl-carrier protein] reductase [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp.  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C:Accession: AH2042  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete genomic sequence of the filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AH2042  
R:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-251 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA073593.1; PID:G17130984; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: fabG  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.6%; Score 333.5; DB 2; Length 251;  
Best Local Similarity 33.1%; Pred. No. 6,8e-19;  
Matches 91; Conservative 46; Mismatches 97; Indels 41; Gaps 7;

QY 1 MAAYRSVKGVAVITGGASGGLTAERLVGGASAVLDD-----VLLDLPNNGG 47  
DB 1 MALLSENLEGGVAVVIGASRGIRALDELANYGATVYVYNASSSTADEVVAETTGAGG 60  
QY 48 EAQAKKLGNNCFAPADVTSEEDVOTATALAKKGRVDVAVNCAGIAVASKTYNLKRGQ 107  
DB 61 EAVALK-----ADVAGVQVONLNGAIDKFRKIDILVNNAGITFDITLLMRK-- 109  
QY 108 TITLDFORLDVNLMTGFNVRIRLVAGEGQNEPPOGGQGVYINTASVAAEFGVGA 167  
DB 110 ----EDWQAVIDLNTGLFGLCTRAVSKMLKQ-----RSGITVITSVAGMGMPGQAN 159  
QY 168 YSASKGIVGMLPIARDLAPIGIRVMTIAPGLFSTPLTSLPEKVCNFLASQVPPSRL 227  
DB 160 YSAKAGVIGFTKTVAKELASRGITVYNAVAPGFIATDMTNNKSE---GIIGYIPL-GRY 215

QY 228 GDPAEYAHLYQALITENP---FLNGEYIRLDGAIIM 259  
DB 216 GQPEELAGMVRFLADPAFAAYITGOVFNVDGGMV 250

RESULT 17  
H84136  
3-oxoacyl-[acyl-carrier protein] reductase BH3896 [imported] - Bacillus halodurans (strain  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: H84136  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: AB3650; MUID:20512582; PMID:11058132  
A:Accession: H84136  
R:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-246 <STO>  
A:Cross-references: GB:AP001520; GB:BA000004; NID:G10176401; PIDN:BA07615.1; GSPDB:GN00  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH3896  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.5%; Score 332; DB 2; Length 246;  
Best Local Similarity 34.2%; Pred. No. 8,7e-19;  
Matches 91; Conservative 40; Mismatches 95; Indels 40; Gaps 8;

RESULT 18  
F82128  
3-oxoacyl-[acyl-carrier-protein] reductase VC2021 [imported] - Vibrio cholerae (str  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C:Accession: F82128  
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gajin, M.L.; Dodson, J.  
Nature 406, 447-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: AB2035; MUID:20406833; PMID:10952301  
A:Accession: F82128  
R:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-248 <HEL>  
A:Cross-references: GB:AE004276; GB:AE003852; NID:9656555; PIDN:AE95169.1; GSPDB:G  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC2021  
A:Map position: 1  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.2%; Score 328.5; DB 2; Length 248;  
Best Local Similarity 32.0%; Pred. No. 1,6e-18;  
Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;

QY 7 SVKGLVAVITGASGLGLTAERLVGGASAVLDDLPNSGGEAOAKKLGNNCFAPADVT 66  
DB 6 NLEGVAVITGASRGIRALDELANYGATVYVYNASSSTADEVVAETTGAGG 65  
QY 67 SEKDVTATLAKKGFGRVDVAVNCAGIAVASKTYNLKGGTHTLDFORLDVNLMTGF 126  
DB 66 NPESEAVLAKITDFGVDLNNAGITRNLMRKE-----EKSIDMETNLSIF 119  
QY 127 NVIRLVAGEGQNEPPOGGQGVYINTASVAAEFGVGAAYSAKGGIVGMLPIARDL 186  
DB 120 RLKRAVLRGMKK-----RGRITVGSVVGTMGNQANVAAKAGVIGFTSMAREV 173  
QY 187 APIGIRVMTIAPGLFSTPLTSLPEKVCNFLASQVPPSRLGDPAEYAHLYQALITENP-- 244  
DB 174 ASRGVAVTVAPGFIETMTKALNDEQFATLADVP-AGRLGDPREIASAV-ATLASPEA 231

QY 245 -FLNGEYIRLDGAIIM 259  
DB 232 AVITGETLHVNGKYM 247

RESULT 19  
E97919  
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [imported] - Streptococcus  
C:Species: Streptococcus pneumoniae

C::Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 02-Nov-2001  
C::Accession: E97919  
R::Hoskins, J.A., Albhorn Jr., W., Arnold, J., Blaszczyk, L., Burgess, S., DeHoff, B.S., F  
er, R., LeBlanc, D.J., Lee, L.N., Lefkowitz, E.J., Lu, J., Matsushima, P., McAhren, S., N  
Y, P., Sun, P.M., Winkler, M.E.  
J::Bacteriol. 183, 5709-5711, 2001  
A::Authors: Yang, Y., Young-Bellido, M., Zhao, G., Zook, C., Baite, R.H., Jaskunas, S.R.,  
A::Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.  
A::Reference number: A97872; MUID:21429245; PMID:11544234  
A::Accession: E97919  
A::Status: Preliminary  
A::Molecule type: DNA  
A::Residues: 1-243 <KUR>  
C::Cross-references: GB:AE007317; PTDN:AAK99185.1; PID:915457942; GSPDB:GN00174  
C::Genes:  
A::Gene: fahb  
C::Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
A::Keywords: oxidoreductase

Query Match	25.0%;	Score	326.5;	DB 2;	Length	243;			
Best Local Similarity	35.1%;	Pred.	No.2,3-18;						
Matches	88;	Conservative	36;	Mismatches	104;	Indels	23;	Gaps	6;

  

QY	15	ITGASGSLGTAERLYVGQGSAYLLDIPNSGGE-----AQAKKLGNCCYFAPADVTSE	68
		:     :     :     :     :     :     :     :	
Db	10	ITGSSRGLGILAIKFAQAGANIVL---NSRGAISELLHEFSNYGKVPISGDSEDF	65
		:     :     :     :     :     :     :     :	
QY	69	KDYVTFATALAKGKRGVDVAVNCAGIAVAASYTNLKKQGTILEDGFCHLVNLNMGTEFNV	128
		:     :     :     :     :     :     :     :	
Db	66	ADAKRMIDQALIAELGSDVLYNNAGI---TQDTLMKMK---TEADFEKVLAVNLTGARNM	119
		:     :     :     :     :     :     :     :	
QY	129	IRLVAEGEGNEDPDQGGRGVIINTASVLAEEGQVGAAYSAGKGIYGMPLPIARDLAP	188
		:     :     :     :     :     :     :     :	
Db	120	TQSVL-----KPMKAREGAIINSSVYVGLMGNGQANVYASKRGLLGFTKSVAREVAS	173
		:     :     :     :     :     :     :     :	
QY	189	IGIRVMTIAPGLFGFPLTSLPERKYCNFLAQGFPSRLGDPAEVAHIVQAAITENPFNG	248
		:     :     :     :     :     :     :     :	
Db	174	RNIHVNVIAIPMIESDMATLISDKIKETALQIPM-KRFGQAQGVADLTVPFLAQQDYLTG	232
		:     :     :     :     :     :     :     :	
QY	249	EVIRLDGAIKM	259
		:     :     :     :     :     :     :     :	
Db	233	QVIAIDGGLSM	243
		:     :     :     :     :     :     :     :	

RESULT 20  
G95048  
3-oxacyl-[acyl-carrier protein] reductase [imported] - Streptococcus pneumoniae (strain  
C:Species: Streptococcus pneumoniae  
C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001  
C:Accession: G95048  
R:Retelstein, H.; Neilson, K.E.; Paulsen, I.T.; Eisen, J.A.; Reed, T.D.; Peterson, S.; Held  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: G95048  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 17243 <KUP>  
A:Cross-references: GB:AE005672; PIDN:AAK74584.1; PID:g14971891; GSPDB:GN00164; TIGR:SP4  
A:Experimental source: Strain TIGR4  
C:Genetics:  
A:Gene: SP0421  
C:Superfamily: rblitol dehydrogenase; short-chain alcohol dehydrogenase homology

```

Query Match      25.0%  Score 325.5  DB 2;  Length 243;
Best Local Similarity 34.7%  Pred. No. 2.8e-18;
Matches      87;  Conservative 37;  Mismatches 104;  Indels 23;  Gaps 6;

09      15 ITGASAGSGLTAEELVGQGSAAVLLDLPNSGGE-----AQAKKLGNCNCFAPADYVSE 68
      ||| : |||| : ||: ||| ||| : | : | ||:

```

```

Db      1  ITSSRGIGTALHKAQGANIYV-----NSRGATSEELLAEFNYNGIKVPIGSDVSE 65
QY      69  KDYQTLALAKRGFGVYVAVNCAGIAAASKTYINLKQQTITLDFQRYLDVNMGVFN 128
Db      66  ADKRMIDQALIELGSDVLYNNAGI--TQDTLMIKM---TEADFEEVLYKNTLGAENM 119
QY      129  IRLVAGEMQNEPDQGGQGVLIINPASAFAEGVGQAAYSASKSGIYGMTLPIARLAP 188
Db      120  TQSVL-----KPMKARREGALINMSVYGLMNGINQANYSAAAGLIGFFKSVAREVAS 173
QY      189  IGIWVITAPGLFGLPLTSLPEKYVCNLSAOVPPPSLGPDAEYAHVQAIINPFLNG 248
Db      174  RNRIVNVIAPGMIESDMTALISDKIKEATLQIIPK-KEFGAEGQVADLVFLAGQDYLTG 232
QY      249  EVIRLDGARIM 259
Db      233  QVVATIDGLISM 243

```

```

RESULT 21
E86721
hypothetical protein fabgl [imported] - Lactococcus lactis subsp. lactis (strain IL14)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: F86721
R:Botolin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; E
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lacti
A:Reference number: AB6625; MUID:21235186; PMID:1137471
A:Accession: F86721
A:status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <STO>
A:Cross-references: GB:AE005176; PID:g12723693; PIDN:AA04872.1; GSPDB:GND0146
A:Experimental source: strain IL1403

```

A:Gene: fabG1  
c:Superfamily: ribitol dehydrogenase, short-chain alcohol dehydrogenase homology  
Query Match 24.9%; Score 324.5; DB 2; Length 243;  
Best Local Similarity 31.7%; Prd. No. 3.3e-18;  
Matches 82; Conservative 46; Mismatches 104; Indels 25; Gaps 6;

```

OY      8 VKGLVAVITGGASGLGIAFAERLYVGAGAVLLDLPNSGGEGOAKKL-----GNNCVF 60
Db      3 IKKNKFNVTYISTGTGIGKALNLOPFAKGSMLIT-----NGRSALISELLAEFTATGAVANG 57
OY      61 APADVTSEKDQOTALALARKGFGRRVDVAVNCAGIAVASKTYLNKKGQTHLEDFOFRLDV 120
Db      58 ISGDISKSEDAKQMVAEALETLLGSVDILNNAGI--TRDGLSKUSE---EDFESYLKI 111
OY      121 NIMGTEFVITLVAGENGQNDPDGGQRGVITMTASVAAPFEGVGQGAASAKSGGIVGNTL 180
Db      112 NLGAEFMTOAVL-----KPMTRASGAILITSSVGLMGAGAGQANAYASAKAGILIGITK 166
OY      181 PIARDLAPIGRVMTIAPGLFTGTPLLTSLPEKYCNFLASQVFPSPRLGDPAEVAHLVOAI 240
Db      166 SIAREVAARVRVNAVAAPFIESDMEVLSDKVKDAMKQGLPM-KRFQMPPEIATATQFL 224
OY      241 IENPFLNGEIVIRLDGAIM 259
Db      225 AEDDEYMTGQVLLTIDGGVSM 243

```

RESULT 22  
D90481  
Hypochemical protein fabg-9 [imported] - Sulfolobus solfataricus  
C.Species: Sulfolobus solfataricus  
C.Date: 24-May-2001 #sequence\_revision 24-May-2001 #ext\_change 15-Jun-2001  
C.Accession: D90481  
R.She, Q.; Singl, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; C  
aret, I.; Jeffries, A.C.; Kezera, C.W.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redda  
arett, R.A.; Ragan, M.A.; SENSE, C.W.; Van der Oost, J.

submitted to GenBank, April 2001  
 A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139  
 A:Accession: D90481  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1799 <KOR>  
 A:Cross-references: GB:AF006641; NID:q13816394; PIDN:AAK43107.1; GSPDB:GN00155  
 C:Genetics:  
 A:Gene: fabG-9  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.3%; Score 317; DB 2; Length 299;  
 Best Local Similarity 32.5%; Pred. No. 1.7e-17;  
 Matches 83; Conservative 47; Mismatches 107; Indels 18; Gaps 5;

12 VAVITGASGLATAERLVGQASAVLLDLPNSG--EAQAARKLNNCFAPADVTSE 68  
 4 VSITGGAKGIGALGYLGRGYAVVADVEAGKRENNHFGEGIDSPFIKTVSSSE 63  
 69 KDVOALALAKGPERGVAVNACINAVASKTYNKKQQTHTLDFORVLDVNLGTFNV 128  
 64 MDVSMKVERVYGRYRIDVNNAGIFSGKSI---EQTLDKMRVITETNLGWLIC 118  
 129 IRLVAGENGONEPDGGRGVINTASVAFEGQVGAAYASAKGIVGMLPIARDLAP 188  
 119 SKYAVKYMKN-----GGVYVNTASTRAFQSEPTBPYSASKGIIATHTSLAVLSK 171  
 169 IGRIMTAPGLFGTPLTSLP-EKVCNPLASQVFFPRRLDPRATVLAQIEN--PF 245  
 172 YNIRVVISIPGWDISPMQVPPRESTLSGLDHGHLTRVRGKEDVASLVTVLSDASW 231  
 246 INGEVIRLDGAIKMQ 260  
 232 ISGVNFTTIDGKMTVK 246

RESULT 23  
 A48154  
 short-chain alcohol dehydrogenase (EC 1.1.1.-) Ke 6 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A48154  
 R:AltZ: N.; Maxwell, M.M.; St. Jacques, B.; Bremer, B.M.  
 Mol. Cell. Biol. 13, 1847-1853, 1993  
 A:Title: Downregulation of Ke 6, a novel gene encoded within the major histocompatibility  
 A:Reference number: A48154; M0ID:93180832; PMID:8441417  
 A:Accession: A48154  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-260 <AZI>  
 A:Cross-references: GB:U34072; NID:q1103843  
 A:Note: sequence extracted from NCBI backbone (NCBIN:126003; NCBI:126004)  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
 C:Keywords: alcohol metabolism; NAD; oxidoreductase  
 F:10-199/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 24.2%; Score 315.5; DB 1; Length 260;  
 Best Local Similarity 31.0%; Pred. No. 1.8e-17;  
 Matches 85; Conservative 55; Mismatches 105; Indels 29; Gaps 9;

1 MAAYRSVKGVAVITGGA-SGLGLATAERLVGQASAVLLDLPNSGGAQAARKLGN--- 56  
 1 MASQLR-IRSAALVTVGGAGSGIGRAISVRLAEGAAYACDDGAADTVYLLGSPSS 59  
 57 -----NCVFPADVTSEKDVDTALALAKGKFG-VDVAVNACIINAVASKTYNKKQ 107  
 60 EDGAPRGKHAAF-QADVSQGPAAARLLEEVQACFSPPVYVSCAGITDEFLLHSE-- 116  
 108 THTLDFORVLDVNLGTFNVIRLVAGENGONEPDGGRGVINTASVAFEGQVGA 167  
 117 -----EDMDRVIAVNIKGTFLVQAQAALVSS-----GGGSIINISIIIGKNGIN 167

QY 168 YSAKSGIYGMTLPARDLAPIGIRVMTAPGLFGTPLTSLPEKVCNPLASQVPPSRU 227  
 168 YASSKAGVIGLITATARELARGHGRICNSVLPGLATIPQKPEKVKDYAMIP--GM 226  
 228 GDPAEYAHLYQ--AIENPFLNGEVIRLDGAIK 259  
 227 GDPEDVADYVAFVASEDSGYITGASVEVSGGLEM 260

RESULT 24  
 T36846  
 probable dehydrogenase - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 11-Jan-2000  
 C:Accession: T36846  
 R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, September 1998  
 A:Reference number: Z21615  
 A:Accession: T36846  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-260 <OLI>  
 A:Cross-references: EMBL:AL031541; PIDN:CAA20822.1; GSPDB:GN00070; SCDDB:SC135.33c  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: SCDDB:SC135.33c  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.2%; Score 315.5; DB 2; Length 260;  
 Best Local Similarity 36.7%; Pred. No. 1.8e-17;  
 Matches 95; Conservative 33; Mismatches 110; Indels 21; Gaps 9;

6 RSVKGLAVITGASGLATAERLVGQASAVLLDLPNSGGEQAARKLNNCFAPADY 65  
 8 RLIVGRVAVVTVGASGIGLATAERLASEGAHVCGDDETRGRAAEETG--TEVQADY 65  
 66 TSEKDVQALALAKGPERGVAVNACINAVASKTYNKKQQTHTLDFORVLDVNLG 125  
 66 TDPEQVEALFPAADITGSDVAFNNAGISPPDDSLTEG---LEAMRGVEVNLTSV 121  
 126 FNVLRLVAGENGONEPDGGRGVINTAS-VAAFEQVGAAYASAKGIVGMLPIAR 184  
 122 YLCKKAALPYKRR---QG--RGSIIIVTASVAMGATSGISTYAKGGLASRELGV 175  
 185 DLAPIGIRVMTAPGLFGTPLTSLP---PEKVCNPLASQVFFSRGDPAEYAHLYQ-- 238  
 176 OFAREGIRVNALCPQVDTPFLRELPAKDPERRARLV-HIPV-CRAFAAEETAAVAF 233  
 239 AIENPFLNGEVIRLDGAI 257  
 234 ASDSSFYVATDFVLDGCI 252

RESULT 25  
 T11579  
 probable short chain alcohol dehydrogenase CPD12, drought-inducible - cowpea  
 C:Species: Vigna unguiculata (cowpea)  
 C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 20-Jun-2000  
 C:Accession: T11579  
 A:Title: Characterization of two cDNAs for novel drought-inducible genes in the hlg1  
 R:Uchida, S.; Yamauchi-Shinozaki, K.; Urao, T.; Shinozaki, K.  
 J. Plant Res. 109, 415-424, 1996  
 A:Reference number: Z17293  
 A:Accession: T11579  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-267 <ITUC>

A:Cross-references: EMBL:D88121  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.2%; Score 315; DB 2; Length 267;  
 Best Local Similarity 34.1%; Pred. No. 2.1e-17;  
 Matches 90; Conservative 45; Mismatches 107; Indels 22; Gaps 6;

Thu Jun 26 06:55:08 2003

us-09-931-186-4.rpr

Page 10

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OY 1 MAAARSVKGLVAVITGGASGLATIAERLVGGSASAVLLDLPNSGGGAOAKKLGNCVF 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LSPVVKRLEGKVAIITGGASGIGETARLFESOHGAHYVADIODVGLSLCNEI-KSAIY 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 61 APADVTSKDVOTATLALAKGKFGHVDVAVNOCAGIAVASKTYNKKGOTHTLEDEFORLIDY 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 VHCYVTKEDIEKCVDTAVSKFGKLDIMFNNAIGDEFK---KSIIDNTKSDPERYISV 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 121 NLMGTFNVIRLVAGEMGONEPDGGRGVIIINTASVAFEGQVGOAAYSASKGGIYGMTL 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 NLVGPFLGTKEAARVM-----IPARRGCIINTASVAGCIGGATHAYTSKHALVGLTK 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 181 PIARDLAPIGIRVMTIAPGLEGTPLT---SLPE---KYCNFLASQVPPPSRLGDPAEY 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 176 NTAVELGOGFIRVNCVSPFAIVTPLLNKYNLDEEGVRYKTYMNLKGYVPVNDVAEALY 235
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OY 234 AHLVOAIIENPFLNGEVIRLDGAI 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 236 L---ASDESKFVSSHNLVIDGGL 255
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Search completed: June 23, 2003, 14:34:18  
Job time : 17.8333 secs

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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:32:58 ; Search time 20.333 Seconds

(Without alignments)  
1388.950 Million cell updates/sec

Title: US-09-931-186-4

Perfect score: 1304

Sequence: 1 MAAVRSVKGLVAVITGAS.....ENPFLNGEYIRLDGAIKMP 261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :  
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2: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep:\*  
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12: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*  
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14: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1299	99.6	261	10	US-09-931-186-8
3	1290	98.9	261	10	US-09-931-186-20
4	1289	98.8	261	10	US-09-931-186-6
5	1289	98.8	261	10	US-09-931-186-23
6	1287	98.7	261	10	US-09-931-186-2
7	1146	87.9	227	9	US-09-984-245-245
8	1146	87.9	227	9	US-09-986-262-245
9	1146	87.9	227	9	US-09-983-966-245
10	1146	87.9	227	9	US-10-143-090-245
11	664.5	51.0	388	9	US-09-920-923-41
12	332.5	25.5	259	10	US-09-931-186-17
13	332.5	25.5	243	10	US-09-815-242-13360
14	326.5	25.0	243	10	US-09-815-242-13581
15	318.5	24.4	243	10	US-09-815-242-10921
16	314	24.1	237	9	US-10-175-696-14
17	314	24.1	237	9	US-09-931-901-2
18	305.5	23.4	253	10	US-09-931-186-15
19	301	23.1	247	9	US-09-479-040-9

20	293.5	22.5	267	9	US-09-773-748-1	Sequence 1, Appl1
21	292.5	22.4	262	9	US-10-307-385-6	Sequence 6, Appl1
22	292.5	22.4	262	10	US-09-802-853-6	Sequence 6, Appl1
23	291.5	22.4	270	9	US-09-978-258A-468	Sequence 468, App
24	291.5	22.4	270	9	US-09-978-597-468	Sequence 468, App
25	291.5	22.4	270	9	US-09-978-192A-468	Sequence 468, App
26	291.5	22.4	270	9	US-09-999-832A-468	Sequence 468, App
27	291.5	22.4	270	9	US-09-978-189A-468	Sequence 468, App
28	291.5	22.4	270	9	US-09-978-508A-468	Sequence 468, App
29	291.5	22.4	270	9	US-09-978-191A-468	Sequence 468, App
30	291.5	22.4	270	9	US-09-978-403A-468	Sequence 468, App
31	291.5	22.4	270	9	US-09-978-564A-468	Sequence 468, App
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33	291.5	22.4	270	9	US-10-017-081A-468	Sequence 468, App
34	291.5	22.4	270	9	US-09-978-82A-468	Sequence 468, App
35	291.5	22.4	270	9	US-09-981-915A-468	Sequence 468, App
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37	291.5	22.4	270	9	US-10-167-749-468	Sequence 468, App
38	291.5	22.4	270	9	US-09-978-585A-468	Sequence 468, App
39	291.5	22.4	270	9	US-09-978-423A-468	Sequence 468, App
40	291.5	22.4	270	9	US-10-013-921A-468	Sequence 468, App
41	291.5	22.4	270	9	US-09-978-193A-468	Sequence 468, App
42	291.5	22.4	270	9	US-10-013-929A-468	Sequence 468, App
43	291.5	22.4	270	9	US-10-015-177A-468	Sequence 468, App
44	291.5	22.4	270	9	US-09-999-830A-468	Sequence 468, App
45	291.5	22.4	270	9	US-09-978-757A-468	Sequence 468, App
46	291.5	22.4	270	9	US-09-978-187B-468	Sequence 468, App
47	291.5	22.4	270	9	US-09-978-643A-468	Sequence 468, App
48	291.5	22.4	270	9	US-10-166-709A-468	Sequence 468, App
49	289.5	22.2	244	10	US-09-815-242-10126	Sequence 10126, A
50	288.5	22.1	642	9	US-09-364-847-59	Sequence 59, Appl1
51	288	22.1	263	10	US-09-815-242-14092	Sequence 14092, A
52	288	22.1	641	9	US-09-364-847-10	Sequence 10, Appl1
53	287.5	22.0	246	9	US-09-364-847-6	Sequence 6, Appl1
54	287.5	22.0	641	9	US-09-364-847-19	Sequence 19, Appl1
55	287.5	22.0	642	9	US-09-364-847-61	Sequence 61, Appl1
56	285.5	21.9	244	9	US-09-849-092-13	Sequence 13, Appl1
57	283.5	21.7	203	9	US-10-175-696-19	Sequence 19, Appl1
58	283.5	21.7	203	10	US-09-823-901-7	Sequence 7, Appl1
59	276	21.2	258	9	US-09-738-620-636	Sequence 646, App
60	274.5	21.1	285	10	US-09-815-242-10241	Sequence 10241, A
61	274.5	21.1	254	9	US-09-978-758-2	Sequence 2, Appl1
62	274	21.0	206	9	US-09-997-816-4	Sequence 4, Appl1
63	273.5	21.0	272	10	US-09-815-242-12688	Sequence 12688, A
64	272.5	20.9	286	10	US-09-815-242-11860	Sequence 11860, A
65	271.5	20.8	251	10	US-09-815-242-5461	Sequence 5461, App
66	269.5	20.7	246	10	US-09-815-242-12123	Sequence 12123, A
67	269.5	20.7	246	10	US-09-815-242-12803	Sequence 12803, A
68	269.5	20.7	246	10	US-09-815-242-13100	Sequence 13100, A
69	269.5	20.6	251	9	US-10-272-419-20	Sequence 20, Appl1
70	268	20.4	242	10	US-09-815-242-10974	Sequence 10974, A
71	266.5	20.4	255	10	US-09-954-314-14	Sequence 14, Appl1
72	266	20.2	276	9	US-09-944-160-24	Sequence 24, Appl1
73	264	20.2	252	9	US-09-910-033A-2	Sequence 2, Appl1
74	262.5	20.1	258	9	US-10-156-055A-1	Sequence 1, Appl1
75	262.5	20.1	253	10	US-09-815-242-11842	Sequence 11842, A
76	259	19.9	261	9	US-09-971-536-74	Sequence 74, Appl1
77	257	19.7	261	9	US-09-940-037A-29	Sequence 29, Appl1
78	254	19.5	261	10	US-09-981-353-40	Sequence 40, Appl1
79	250.5	19.2	266	9	US-09-885-823A-72	Sequence 72, App
80	250.5	19.2	266	9	US-10-205-823-176	Sequence 176, App
81	250.5	19.2	266	10	US-09-931-186-18	Sequence 18, Appl1
82	250.5	19.2	266	10	US-09-764-853-553	Sequence 553, App
83	250	19.2	221	10	US-09-815-242-10597	Sequence 10597, A
84	245.5	18.8	262	10	US-09-815-242-10846	Sequence 10846, A
85	242.5	18.6	261	10	US-09-923-501-16	Sequence 16, Appl1
86	241	18.5	251	10	US-09-931-186-14	Sequence 14, Appl1
87	239	18.3	255	10	US-09-815-242-11893	Sequence 11893, A
88	238	18.3	247	10	US-09-954-314-12	Sequence 12, Appl1
89	237.5	18.2	274	9	US-09-976-059-17	Sequence 17, Appl1
90	235	18.0	271	10	US-09-815-242-13387	Sequence 13387, A
91	235	18.0	271	10	US-09-815-242-13679	Sequence 13679, A
92	235	18.0	272	10	US-09-815-242-13679	Sequence 13679, A

93 233 17.9 311 9 US-09-738-626-3819 Sequence 3819, Ap  
94 232 17.8 261 10 US-09-815-242-5813 Sequence 5813, Ap  
95 225.5 17.3 247 10 US-09-815-242-11342 Sequence 11342, A  
96 224 17.2 254 10 US-09-741-669-411 Sequence 411, App  
97 222.5 17.1 247 10 US-09-815-242-11514 Sequence 11514, A  
98 222.5 17.1 900 9 US-10-060-230-15 Sequence 15, Appl  
99 222.5 17.1 900 9 US-10-060-230-17 Sequence 17, Appl  
100 216.5 16.6 253 10 US-09-815-242-10279 Sequence 10279, A

## ALIGNMENTS

RESULT 1  
US-09-931-186-4  
Sequence 4, Application US/09931186  
Patent No. US20020132319A1  
GENERAL INFORMATION:  
APPLICANT: AGREE, CHARLES S.  
APPLICANT: AUST, ROBERT  
APPLICANT: KISSINGER, CHARLES R.  
APPLICANT: MARGOSIAK, STEVE  
APPLICANT: MENG, JERRY J.  
APPLICANT: PELLETIER, LAURA A.  
APPLICANT: REJTO, PAUL A.  
APPLICANT: SHOWALTER, RICHARD E.  
APPLICANT: TEMPCEZYK-RUSSELL, ANNA  
APPLICANT: THOMSON, JIM  
APPLICANT: VANDERPOOL, DARIN  
APPLICANT: VILLAFRANCA, J. ERNEST  
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL  
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION  
FILE REFERENCE: 0125-0049  
CURRENT APPLICATION NUMBER: US/09/931,186  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 261  
TYPE: PRP  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: full length mutant ERAB CSV  
US-09-931-186-4  
Query Match 100.0%; Score 1304; DB 10; Length 261;  
Best Local Similarity 100.0%; Pred. No. 3.1e-110;  
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 241 IENPFLNGEIVIRLDGAIRMOP 261  
DB 241 IENPFLNGEIVIRLDGAIRMOP 261

US-09-931-186-8  
Sequence 8, Application US/09931186  
Patent No. US20020132319A1  
GENERAL INFORMATION:  
APPLICANT: AGREE, CHARLES S.  
APPLICANT: AUST, ROBERT  
APPLICANT: KISSINGER, CHARLES R.  
APPLICANT: MARGOSIAK, STEVE  
APPLICANT: MENG, JERRY J.  
APPLICANT: PELLETIER, LAURA A.  
APPLICANT: REJTO, PAUL A.  
APPLICANT: SHOWALTER, RICHARD E.  
APPLICANT: TEMPCEZYK-RUSSELL, ANNA  
APPLICANT: THOMSON, JIM  
APPLICANT: VANDERPOOL, DARIN  
APPLICANT: VILLAFRANCA, J. ERNEST  
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL  
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION  
FILE REFERENCE: 0125-0049  
CURRENT APPLICATION NUMBER: US/09/931,186  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 261  
TYPE: PRP  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: wild type ERAB  
US-09-931-186-8  
Query Match 99.6%; Score 1299; DB 10; Length 261;  
Best Local Similarity 99.6%; Pred. No. 8.9e-110;  
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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QY 241 IENPFLNGEIVIRLDGAIRMOP 261  
DB 241 IENPFLNGEIVIRLDGAIRMOP 261

RESULT 2